

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: BROW, MARY ANN D.
LYAMICHEV, VICTOR I.
OLIVE, DAVID M.
- (ii) TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF PATHOGENS
- (iii) NUMBER OF SEQUENCES: 160
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: MEDLEN & CARROLL
 - (B) STREET: 220 MONTGOMERY STREET, SUITE 2200
 - (C) CITY: SAN FRANCISCO
 - (D) STATE: CALIFORNIA
 - (E) COUNTRY: UNITED STATES OF AMERICA
 - (F) ZIP: 94104
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: CARROLL, PETER G.
 - (B) REGISTRATION NUMBER: 32,837
 - (C) REFERENCE/DOCKET NUMBER: FORS-01756
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (415) 705-8410
 - (B) TELEFAX: (415) 397-8338

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2506 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAGGGGGA TGCTGCCCCCT CTTTGAGCCC AAGGGCCGGG TCCTCCTGGT GGACGGCCAC	60
CACCTGGCCT ACCGCACCTT CCACGCCCTG AAGGGCCTCA CCACCAGCCG GGGGGAGCCG	120
GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTCAAGGA GGACGGGGAC	180
GCGGTGATCG TGGTCTTTGA CGCCAAGGCC CCCTCCTTCC GCCACGAGGC CTACGGGGGG	240
TACAAGGCGG GCCGGGCCCC CACGCCGGAG GACTTTCCCC GGCAACTCGC CCTCATCAAG	300

GAGCTGGTGG ACCTCCTGGG GCTGGCGCGC CTCGAGGTCC CGGGCTACGA GGCGGACGAC	360
GTCCTGGCCA GCCTGGCCAA GAAGGCGGAA AAGGAGGGCT ACGAGGTCCG CATCCTCACC	420
GCCGACAAAG ACCTTTACCA GCTCCTTTCC GACCGCATCC ACGTCCTCCA CCCCAGAGGG	480
TACCTCATCA CCCCAGCCTG GCTTTGGGAA AAGTACGGCC TGAGGCCCCGA CCAGTGGGCC	540
GACTACCGGG CCCTGACCGG GGACGAGTCC GACAACCTTC CCGGGGTCAA GGGCATCGGG	600
GAGAAGACGG CGAGGAAGCT TCTGGAGGAG TGGGGGAGCC TGGAAGCCCT CCTCAAGAAC	660
CTGGACCGGC TGAAGCCCGC CATCCGGGAG AAGATCCTGG CCCACATGGA CGATCTGAAG	720
CTCTCCTGGG ACCTGGCCAA GGTGCGCACC GACCTGCCCC TGGAGGTGGA CTTGCCCCAA	780
AGGCGGGAGC CCGACCGGA GAGGCTTAGG GCCTTTCTGG AGAGGCTTGA GTTTGGCAGC	840
CTCTCCACG AGTTCGGCCT TCTGGAAAGC CCCAAGGCC TGGAGGAGGC CCCCTGGCCC	900
CCGCCGGAAG GGGCCTTCGT GGGCTTTGTG CTTTCCCCGA AGGAGCCCAT GTGGGCCGAT	960
CTTCTGGCCC TGGCCGCCG CAGGGGGGGC CGGGTCCACC GGGCCCCCGA GCCTTATAAA	1020
GCCCTCAGGG ACCTGAAGGA GGCGCGGGGG CTTCTCGCCA AAGACCTGAG CGTTCTGGCC	1080
CTGAGGGAAG GCCTTGCCCT CCCGCCCCGGC GACGACCCCA TGCTCCTCGC CTACCTCCTG	1140
GACCCTTCCA ACACCACCCC CGAGGGGGTG GCCCGGCGCT ACGGCGGGGA GTGGACGGAG	1200
GAGGCGGGGG AGCGGGCCGC CCTTTCCGAG AGGCTCTTCG CCAACCTGTG GGGGAGGCTT	1260
GAGGGGGAGG AGAGGCTCCT TTGGCTTTAC CGGGAGGTGG AGAGGCCCTT TTCCGCTGTC	1320
CTGGCCCACA TGGAGGCCAC GGGGGTGCGC CTGGACGTGG CTTATCTCAG GGCTTGTCE	1380
CTGGAGGTGG CCGAGGAGAT CGCCCGCCTC GAGGCCGAGG TCTTCCGCCT GGCCGGCCAC	1440
CCCTTCAACC TCAACTCCCG GGACCAGCTG GAAAGGGTCC TCTTTGACGA GCTAGGGCTT	1500
CCCGCCATCG GCAAGACGGA GAAGACCGGC AAGCGCTCCA CCAGCGCCGC CGTCCTGGAG	1560
GCCCTCCGCG AGGCCACCCC CATCGTGGAG AAGATCCTGC AGTACCGGA GCTCACCAAG	1620
CTGAAGAGCA CTTACATTGA CCCCTTGCCG GACCTCATCC ACCCCAGGAC GGGCCGCCTC	1680
CACACCCGCT TCAACCAGAC GGCCACGGCC ACGGGCAGGC TAAGTAGCTC CGATCCCAAC	1740
CTCCAGAACA TCCCCGTCCG CACCCCGCTT GGGCAGAGGA TCCGCCGGGC CTTTCATCGCC	1800
GAGGAGGGGT GGCTATTGGT GGCCCTGGAC TATAGCCAGA TAGAGCTCAG GGTGCTGGCC	1860
CACCTCTCCG GCGACGAGAA CTTGATCCGG GTCTTCCAGG AGGGGCGGGA CATCCACACG	1920
GAGACCGCCA GCTGGATGTT CGGCGTCCCC CGGGAGGCCG TGGACCCCT GATGCGCCGG	1980
GCGGCCAAGA CCATCAACTT CGGGGTCTC TACGGCATGT CGGCCACCG CCTCTCCAG	2040
GAGCTAGCCA TCCCTTACGA GGAGGCCAG GCCTTCATTG AGCGCTACTT TCAGAGCTTC	2100
CCCAAGGTGC GGGCCTGGAT TGAGAAGACC CTGGAGGAGG GCAGGAGGCG GGGGTACGTG	2160

GAGACCCTCT TCGGCCGCCG CCGCTACGTG CCAGACCTAG AGGCCCGGGT GAAGAGCGTG 2220
 CGGGAGGCGG CCGAGCGCAT GGCCTTCAAC ATGCCCCTCC AGGGCACCGC CGCCGACCTC 2280
 ATGAAGCTGG CTATGGTGAA GCTCTTCCCC AGGCTGGAGG AAATGGGGGC CAGGATGCTC 2340
 CTTCAGGTCC ACGACGAGCT GGTCTCGAG GCCCCAAAAG AGAGGGCGGA GGCCGTGGCC 2400
 CGGCTGGCCA AGGAGGTCAT GGAGGGGGTG TATCCCCTGG CCGTGCCCCT GGAGGTGGAG 2460
 GTGGGGATAG GGGAGGACTG GCTCTCCGCC AAGGAGTGAT ACCACC 2506

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGGCGATGC TTCCCCTCTT TGAGCCCAA GGCCGCGTGC TCCTGGTGA CGGCCACCAC 60
 CTGGCCTACC GCACCTTCTT TGCCCTCAAG GGCCTCACCA CCAGCCGCGG CGAACCCGTT 120
 CAGGCGGTCT ACGGCTTCGC CAAAAGCCTC CTCAAGGCC TGAAGGAGGA CGGGGACGTG 180
 GTGGTGGTGG TCTTTGACGC CAAGGCCCC TCCTTCCGCC ACGAGGCCTA CGAGGCCTAC 240
 AAGGCGGGCC GGGCCCCAC CCCGAGGAC TTTCCC CGG AGCTGGCCCT CATCAAGGAG 300
 TTGGTGGACC TCCTAGGCCCT TGTGCGGCTG GAGGTTCCCG GCTTTGAGGC GGACGACGTG 360
 CTGGCCACCC TGGCCAAGCG GGCGGAAAAG GAGGGGTACG AGGTGCGCAT CCTCACTGCC 420
 GACCGCGACC TCTACCAGCT CCTTTCGGAG CGCATCGCCA TCCTCCACCC TGAGGGGTAC 480
 CTGATCACCC CGGCGTGGCT TTACGAGAAG TACGGCCTGC GCCCGGAGCA GTGGGTGGAC 540
 TACCGGGCCC TGGCGGGGGA CCCCTCGGAT AACATCCCCG GGGTGAAGGG CATCGGGGAG 600
 AAGACCGCCC AGAGGCTCAT CCGCGAGTGG GGGAGCCTGG AAAACCTCTT CCAGCACCTG 660
 GACCAGGTGA AGCCCTCCTT GCGGGAGAAG CTCCAGGCGG GCATGGAGGC CCTGGCCCTT 720
 TCCCGGAAGC TTTCCCAGGT GCACACTGAC CTGCCCCCTGG AGGTGGACTT CGGGAGGCGC 780
 CGCACACCCA ACCTGGAGGG TCTGCGGGCT TTTTGGAGC GGTGGAGTT TGGAAGCCTC 840
 CTCCACGAGT TCGGCCTCCT GGAGGGGCGG AAGGCGGCAG AGGAGGCCCC CTGGCCCCCT 900
 CCGGAAGGGG CTTTTTTGGG CTTTTCCTTT TCCCGTCCCG AGCCCATGTG GGCCGAGCTT 960
 CTGGCCCTGG CTGGGGCGTG GGAGGGGCGC CTCCATCGGG CACAAGACCC CCTTAGGGGC 1020
 CTGAGGGACC TTAAGGGGGT GCGGGGAATC CTGGCCAAGG ACCTGGCGGT TTTGGCCCTG 1080
 CGGGAGGGCC TGGACCTCTT CCCAGAGGAC GACCCCATGC TCCTGGCCTA CCTTCTGGAC 1140

CCCTCCAACA CCACCCCTGA GGGGGTGGCC CGGCGTTACG GGGGGGAGTG GACGGAGGAT	1200
GCGGGGGAGA GGGCCCTCCT GGCCGAGCGC CTCTTCCAGA CCCTAAAGGA GCGCCTTAAG	1260
GGAGAAGAAC GCCTGCTTTG GCTTTACGAG GAGGTGGAGA AGCCGCTTTC CCGGGTGTG	1320
GCCCGGATGG AGGCCACGGG GGTCCGGCTG GACGTGGCCT ACCTCCAGGC CCTCTCCCTG	1380
GAGGTGGAGG CGGAGGTGCG CCAGCTGGAG GAGGAGGTCT TCCGCTGGC CGGCCACCCC	1440
TTCAACCTCA ACTCCCGCGA CCAGCTGGAG CGGGTGCTCT TTGACGAGCT GGGCCTGCCT	1500
GCCATCGGCA AGACGGAGAA GACGGGGAAA CGCTCCACCA GCGCTGCCGT GCTGGAGGCC	1560
CTGCGAGAGG CCCACCCCAT CGTGGACCGC ATCCTGCAGT ACCGGGAGCT CACCAAGCTC	1620
AAGAACACCT ACATAGACCC CCTGCCCCGCC CTGGTCCACC CCAAGACCGG CCGGCTCCAC	1680
ACCCGCTTCA ACCAGACGGC CACCGCCACG GGCAGGCTTT CCAGCTCCGA CCCCAACCTG	1740
CAGAACATCC CCGTGCGCAC CCCTCTGGGC CAGCGCATCC GCCGAGCCTT CGTGGCCGAG	1800
GAGGGCTGGG TGCTGGTGGT CTGGACTAC AGCCAGATTG AGCTTCGGGT CCTGGCCCAC	1860
CTCTCCGGGG ACGAGAACCT GATCCGGGTC TTTCAGGAGG GGAGGGACAT CCACACCCAG	1920
ACCGCCAGCT GGATGTTCCG CGTTTCCCCC GAAGGGGTAG ACCCTCTGAT GCGCCGGGCG	1980
GCCAAGACCA TCAACTTCGG GGTGCTCTAC GGCATGTCCG CCCACCGCCT CTCCGGGGAG	2040
CTTTCCATCC CCTACGAGGA GGCGGTGGCC TTCATTGAGC GCTACTTCCA GAGCTACCCC	2100
AAGGTGCGGG CCTGGATTGA GGGGACCCTC GAGGAGGGCC GCCGGCGGGG GTATGTGGAG	2160
ACCCTCTTCG GCCGCCGGCG CTATGTGCCC GACCTCAACG CCCGGGTGAA GAGCGTGCGE	2220
GAGGCGGCGG AGCGCATGGC CTTCAACATG CCGTCCAGG GCACCGCCGC CGACCTCATG	2280
AAGCTGGCCA TGGTGGGCT TTTCCCCCGG CTTCAGGAAC TGGGGGCGAG GATGCTTTTG	2340
CAGGTGCACG ACGAGCTGGT CCTCGAGGCC CCCAAGGACC GGGCGGAGAG GGTAGCCGCT	2400
TTGGCCAAGG AGGTCATGGA GGGGGTCTGG CCCCTGCAGG TGCCCCTGGA GGTGGAGGTG	2460
GGCCTGGGGG AGGACTGGCT CTCCGCCAAG GAGTAG	2496

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGAGGCGA TGCTTCCGCT CTTTGAACCC AAAGGCCGGG TCCTCCTGGT GGACGGCCAC	60
CACCTGGCCT ACCGCACCTT CTTCGCCCTG AAGGGCCTCA CCACGAGCCG GGGCGAACCG	120

GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTGAAGGA GGACGGGTAC	180
AAGGCCGTCT TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGAG	240
GCCTACAAGG CGGGGAGGGC CCCGACCCCC GAGGACTTCC CCCGGCAGCT CGCCCTCATC	300
AAGGAGCTGG TGGACCTCCT GGGGTTTACC CGCCTCGAGG TCCCCGGCTA CGAGGCGGAC	360
GACGTTCTCG CCACCCCTGGC CAAGAAGGCG GAAAAGGAGG GGTACGAGGT GCGCATCCTC	420
ACCGCCGACC GCGACCTCTA CCAACTCGTC TCCGACCGCG TCGCCGTCCT CCACCCCGAG	480
GGCCACCTCA TCACCCCGGA GTGGCTTTGG GAGAAGTACG GCCTCAGGCC GGAGCAGTGG	540
GTGGACTTCC GCGCCCTCGT GGGGGACCCC TCCGACAACC TCCCCGGGGT CAAGGGCATC	600
GGGGAGAAGA CCGCCCTCAA GCTCCTCAAG GAGTGGGGAA GCCTGGAAAA CCTCCTCAAG	660
AACCTGGACC GGGTAAAGCC AGAAAACGTC CGGGAGAAGA TCAAGGCCCA CCTGGAAGAC	720
CTCAGGCTCT CTTTGGAGCT CTCCCGGGTG CGCACCGACC TCCCCCTGGA GGTGGACCTC	780
GCCCAGGGGC GGGAGCCCGA CCGGGAGGGG CTTAGGGCCT TCCTGGAGAG GCTGGAGTTC	840
GGCAGCCTCC TCCACGAGTT CGGCCTCCTG GAGGCCCCCG CCCCCCTGGA GGAGGCCCCC	900
TGGCCCCCGC CGGAAGGGGC CTTCGTGGGC TTCGTCCTCT CCCGCCCGGA GCCCATGTGG	960
GCGGAGCTTA AAGCCCTGGC CGCCTGCAGG GACGGCCGGG TGCACCGGGC AGCAGACCCC	1020
TTGGCGGGGC TAAAGGACCT CAAGGAGGTC CGGGGCCTCC TCGCCAAGGA CCTCGCCGTC	1080
TTGGCCTCGA GGGAGGGGCT AGACCTCGTG CCCGGGGACG ACCCCATGCT CCTCGCCTAC	1140
CTCCTGGACC CCTCCAACAC CACCCCCGAG GGGGTGGCGC GCGCTACGG GGGGGAGTGG	1200
ACGGAGGACG CCGCCCACCG GGCCCTCCTC TCGGAGAGGC TCCATCGGAA CCTCCTTAAG	1260
CGCCTCGAGG GGGAGGAGAA GCTCCTTTGG CTCTACCAG AGGTGGAAAA GCCCCTCTCC	1320
CGGGTCCTGG CCCACATGGA GGCCACCGGG GTACGGCTGG ACGTGGCCTA CCTTCAGGCC	1380
CTTTCCCTGG AGCTTGCGGA GGAGATCCGC CGCCTCGAGG AGGAGGTCTT CCGCTTGGCG	1440
GGCCACCCCT TCAACCTCAA CTCCCGGGAC CAGCTGGAAA GGGTGCTCTT TGACGAGCTT	1500
AGGCTTCCCG CTTTGGGGAA GACGCAAAAG ACAGGCAAGC GCTCCACCAG CGCCGCGGTG	1560
CTGGAGGCCC TACGGGAGGC CCACCCCATC GTGGAGAAGA TCCTCCAGCA CCGGGAGCTC	1620
ACCAAGCTCA AGAACACCTA CGTGGACCCC CTCCCAAGCC TCGTCCACCC GAGGACGGGC	1680
CGCCTCCACA CCCGCTTCAA CCAGACGGCC ACGGCCACGG GGAGGCTTAG TAGCTCCGAC	1740
CCCAACCTGC AGAACATCCC CGTCCGCACC CCCTTGGGCC AGAGGATCCG CCGGGCCTTC	1800
GTGGCCGAGG CGGGTTGGGC GTTGGTGGCC CTGGACTATA GCCAGATAGA GCTCCGCGTC	1860
CTCGCCACC TCTCCGGGGA CGAAAACCTG ATCAGGGTCT TCCAGGAGGG GAAGGACATC	1920
CACACCCAGA CCGCAAGCTG GATGTTTCGGC GTCCCCCGG AGGCCGTGGA CCCCCTGATG	1980

CGCCGGGCGG CCAAGACGGT GAACTTCGGC GTCCTCTACG GCATGTCCGC CCATAGGCTC 2040
 TCCCAGGAGC TTGCCATCCC CTACGAGGAG GCGGTGGCCT TTATAGAGGC TACTTCCAAA 2100
 GCTTCCCCAA GGTGCGGGCC TGGATAGAAA AGACCCTGGA GGAGGGGAGG AAGCGGGGCT 2160
 ACGTGGAAC CCTCTTCGGA AGAAGGCGCT ACGTGCCCGA CCTCAACGCC CGGGTGAAGA 2220
 GCGTCAGGGA GGCCGCGGAG CGCATGGCCT TCAACATGCC CGTCCAGGGC ACCGCCGCCG 2280
 ACCTCATGAA GCTCGCCATG GTGAAGCTCT TCCCCGCCT CCGGGAGATG GGGGCCCGCA 2340
 TGCTCCTCCA GGTCCACGAC GAGCTCCTCC TGGAGGCCCC CCAAGCGCGG GCCGAGGAGG 2400
 TGGCGGCTTT GGCCAAGGAG GCCATGGAGA AGGCCTATCC CCTCGCCGTG CCCCTGGAGG 2460
 TGGAGGTGGG GATGGGGGAG GACTGGCTTT CCGCCAAGGG TTAG 2504

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 832 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu
 1 5 10 15
 Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly
 20 25 30
 Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
 35 40 45
 Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val
 50 55 60
 Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly
 65 70 75 80
 Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu
 85 90 95
 Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu
 100 105 110
 Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys
 115 120 125
 Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp
 130 135 140
 Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly
 145 150 155 160
 Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro
 165 170 175

Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	Asn	
			180					185					190			
Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	Leu	
		195					200					205				
Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	Leu	
		210				215					220					
Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	Lys	
225					230					235					240	
Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	Val	
				245					250					255		
Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala	Phe	
			260					265					270			
Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	Leu	
		275					280					285				
Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly	
		290				295					300					
Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala	Asp	
305					310					315					320	
Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala	Pro	
				325					330					335		
Glu	Pro	Tyr	Lys	Ala	Leu	Arg	Asp	Leu	Lys	Glu	Ala	Arg	Gly	Leu	Leu	
			340					345					350			
Ala	Lys	Asp	Leu	Ser	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Gly	Leu	Pro	
		355					360					365				
Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	Asn	
		370				375					380					
Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	Glu	
385					390					395					400	
Glu	Ala	Gly	Glu	Arg	Ala	Ala	Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn	Leu	
				405					410					415		
Trp	Gly	Arg	Leu	Glu	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg	Glu	
			420					425					430			
Val	Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr	Gly	
		435					440					445				
Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val	Ala	
		450				455					460					
Glu	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly	His	
465					470					475					480	
Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	Asp	
				485					490					495		
Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	Arg	
			500					505					510			

Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	Ile
		515					520					525			
Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser	Thr
	530					535					540				
Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg	Leu
545					550					555					560
His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser
				565					570					575	
Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln
			580					585					590		
Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val	Ala
		595					600					605			
Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly
	610					615					620				
Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	Thr
625					630					635					640
Glu	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	Pro
				645					650					655	
Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	Gly
			660					665					670		
Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	Glu
		675					680					685			
Ala	Gln	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	Arg
	690					695					700				
Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	Val
705					710					715					720
Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Glu	Ala	Arg
				725					730					735	
Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro
			740					745					750		
Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	Leu
		755					760					765			
Phe	Pro	Arg	Leu	Glu	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	His
	770					775					780				
Asp	Glu	Leu	Val	Leu	Glu	Ala	Pro	Lys	Glu	Arg	Ala	Glu	Ala	Val	Ala
785					790					795					800
Arg	Leu	Ala	Lys	Glu	Val	Met	Glu	Gly	Val	Tyr	Pro	Leu	Ala	Val	Pro
				805					810					815	
Leu	Glu	Val	Glu	Val	Gly	Ile	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	Glu
			820					825					830		

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 831 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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Met Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
1           5           10           15
Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu
          20           25           30
Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
          35           40           45
Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Val Val Val Val Val
          50           55           60
Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala Tyr
          65           70           75           80
Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
          85           90           95
Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Val Arg Leu Glu Val
          100          105          110
Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Arg Ala
          115          120          125
Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu
          130          135          140
Tyr Gln Leu Leu Ser Glu Arg Ile Ala Ile Leu His Pro Glu Gly Tyr
          145          150          155          160
Leu Ile Thr Pro Ala Trp Leu Tyr Glu Lys Tyr Gly Leu Arg Pro Glu
          165          170          175
Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile
          180          185          190
Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Gln Arg Leu Ile Arg
          195          200          205
Glu Trp Gly Ser Leu Glu Asn Leu Phe Gln His Leu Asp Gln Val Lys
          210          215          220
Pro Ser Leu Arg Glu Lys Leu Gln Ala Gly Met Glu Ala Leu Ala Leu
          225          230          235          240
Ser Arg Lys Leu Ser Gln Val His Thr Asp Leu Pro Leu Glu Val Asp
          245          250          255
Phe Gly Arg Arg Arg Thr Pro Asn Leu Glu Gly Leu Arg Ala Phe Leu
          260          265          270
Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu

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275					280					285					
Gly	Pro	Lys	Ala	Ala	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly	Ala
290					295					300					
Phe	Leu	Gly	Phe	Ser	Phe	Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala	Glu	Leu
305					310					315					320
Leu	Ala	Leu	Ala	Gly	Ala	Trp	Glu	Gly	Arg	Leu	His	Arg	Ala	Gln	Asp
				325					330					335	
Pro	Leu	Arg	Gly	Leu	Arg	Asp	Leu	Lys	Gly	Val	Arg	Gly	Ile	Leu	Ala
			340					345					350		
Lys	Asp	Leu	Ala	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Asp	Leu	Phe	Pro
		355					360					365			
Glu	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	Asn	Thr
	370					375					380				
Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	Glu	Asp
385					390					395					400
Ala	Gly	Glu	Arg	Ala	Leu	Leu	Ala	Glu	Arg	Leu	Phe	Gln	Thr	Leu	Lys
				405					410					415	
Glu	Arg	Leu	Lys	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Glu	Glu	Val
			420					425					430		
Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	Arg	Met	Glu	Ala	Thr	Gly	Val
		435					440					445			
Arg	Leu	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser	Leu	Glu	Val	Glu	Ala
	450					455					460				
Glu	Val	Arg	Gln	Leu	Glu	Glu	Val	Phe	Arg	Leu	Ala	Gly	His	Pro	
465				470					475					480	
Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	Asp	Glu
				485					490					495	
Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	Arg	Ser
			500				505						510		
Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	Ile	Val
		515					520					525			
Asp	Arg	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Asn	Thr	Tyr
	530					535					540				
Ile	Asp	Pro	Leu	Pro	Ala	Leu	Val	His	Pro	Lys	Thr	Gly	Arg	Leu	His
545				550						555				560	
Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser
				565					570					575	
Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln	Arg
			580				585						590		
Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Glu	Gly	Trp	Val	Leu	Val	Val	Leu
		595					600					605			

Asp 610	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly	Asp
Glu 625	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	Thr	Gln 640
Thr	Ala	Ser	Trp	Met 645	Phe	Gly	Val	Ser	Pro 650	Glu	Gly	Val	Asp	Pro 655	Leu
Met	Arg	Arg	Ala 660	Ala	Lys	Thr	Ile	Asn 665	Phe	Gly	Val	Leu	Tyr 670	Gly	Met
Ser	Ala 675	His	Arg	Leu	Ser	Gly	Glu 680	Leu	Ser	Ile	Pro	Tyr 685	Glu	Glu	Ala
Val 690	Ala	Phe	Ile	Glu	Arg	Tyr 695	Phe	Gln	Ser	Tyr	Pro 700	Lys	Val	Arg	Ala
Trp 705	Ile	Glu	Gly	Thr	Leu 710	Glu	Glu	Gly	Arg	Arg 715	Arg	Gly	Tyr	Val	Glu 720
Thr	Leu	Phe	Gly	Arg 725	Arg	Arg	Tyr	Val	Pro 730	Asp	Leu	Asn	Ala	Arg 735	Val
Lys	Ser	Val	Arg 740	Glu	Ala	Ala	Glu	Arg 745	Met	Ala	Phe	Asn	Met 750	Pro	Val
Gln	Gly	Thr 755	Ala	Ala	Asp	Leu	Met 760	Lys	Leu	Ala	Met	Val 765	Arg	Leu	Phe
Pro 770	Arg	Leu	Gln	Glu	Leu	Gly 775	Ala	Arg	Met	Leu	Leu 780	Gln	Val	His	Asp
Glu 785	Leu	Val	Leu	Glu	Ala 790	Pro	Lys	Asp	Arg	Ala 795	Glu	Arg	Val	Ala	Ala 800
Leu	Ala	Lys	Glu	Val 805	Met	Glu	Gly	Val	Trp 810	Pro	Leu	Gln	Val	Pro 815	Leu
Glu	Val	Glu	Val 820	Gly	Leu	Gly	Glu	Asp 825	Trp	Leu	Ser	Ala	Lys 830	Glu	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu
1				5					10					15	
Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly
			20					25					30		
Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala
		35				40						45			

Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	Val	Phe
50							55							60	
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Glu
65					70					75					80
Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	Pro	Glu
145					150					155					160
Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
			165						170					175	
Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	Ser	Asp
			180					185					190		
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	Lys	Leu
		195					200					205			
Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	Asp	Arg
	210					215					220				
Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu	Glu	Asp
225					230					235					240
Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu	Pro	Leu
				245					250					255	
Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Arg
			260					265					270		
Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly
		275					280					285			
Leu	Leu	Glu	Ala	Pro	Ala	Pro	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro
		290				295					300				
Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp
305					310					315					320
Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys	Arg	Asp	Gly	Arg	Val	His	Arg
				325					330					335	
Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val	Arg	Gly
			340					345					350		
Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly	Leu	Asp
		355					360					365			
Leu	Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro
						375					380				

Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
385 390 395 400

Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
405 410 415

Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
420 425 430

His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
435 440 445

Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
450 455 460

Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala
465 470 475 480

Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
485 490 495

Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys Thr Gly
500 505 510

Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
515 520 525

Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
530 535 540

Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly
545 550 555 560

Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
565 570 575

Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
580 585 590

Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
595 600 605

Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
610 615 620

Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
625 630 635 640

His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
645 650 655

Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
660 665 670

Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
675 680 685

Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
690 695 700

Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
705 710 715 720

Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
725 730 735

Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
740 745 750

Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
755 760 765

Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
770 775 780

Val His Asp Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
785 790 795 800

Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
805 810 815

Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
820 825 830

Lys Gly

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2502 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGNNGGCGA TGCTTCCCCCT CTTTGAGCCC AAAGGCCGGG TCCTCCTGGT GGACGGCCAC	60
CACCTGGCCT ACCGCACCTT CTTCGCCCTG AAGGGCCTCA CCACCAGCCG GGGCGAACCG	120
GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTGAAGGA GGACGGGGAC	180
NNGGCGGTGN TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGAG	240
GCCTACAAGG CGGGCCGGGC CCCCACCCCG GAGGACTTTC CCCGGCAGCT CGCCCTCATC	300
AAGGAGCTGG TGGACCTCCT GGGGCTTGCG CGCCTCGAGG TCCCCGGCTA CGAGGCGGAC	360
GACGTNCTGG CCACCCTGGC CAAGAAGGCG GAAAAGGAGG GGTACGAGGT GCGCATCCTC	420
ACCGCCGACC GCGACCTCTA CCAGCTCCTT TCCGACCGCA TCGCCGTCCT CCACCCCGAG	480
GGGTACCTCA TCACCCCGGC GTGGCTTTGG GAGAAGTACG GCCTGAGGCC GGAGCAGTGG	540
GTGGACTACC GGGCCCTGGC GGGGGACCCC TCCGACAACC TCCCCGGGGT CAAGGGCATC	600
GGGGAGAAGA CCGCCCNAA GCTCCTCNAG GAGTGGGGGA GCCTGGAAAA CCTCCTCAAG	660
AACCTGGACC GGGTGAAGCC CGCCNTCCGG GAGAAGATCC AGGCCACAT GGANGACCTG	720
ANGCTCTCCT GGGAGCTNTC CCAGGTGCGC ACCGACCTGC CCCTGGAGGT GGACTTCGCC	780
AAGNGCGGG AGCCCGACCG GGAGGGGCTT AGGGCCTTTC TGGAGAGGCT GGAGTTTGCC	840

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AGCCTCCTCC ACGAGTTCGG CTCCTGGAG GGGCCCAAGG CCCTGGAGGA GGCCCCCTGG      900
CCCCCGCCGG AAGGGGCCTT CGTGGGCTTT GTCCCTTTCCC GCCCCGAGCC CATGTGGGGCC      960
GAGCTTCTGG CCCTGGCCGC CGCCAGGGAG GGCCGGGTCC ACCGGGCACC AGACCCCTTT      1020
ANGGGCCTNA GGGACCTNAA GGAGGTGCGG GGNCCTCTCG CCAAGGACCT GGCCGTTTTG      1080
GCCCTGAGGG AGGGCCTNGA CCTCNTGCCC GGGGACGACC CCATGCTCCT CGCCTACCTC      1140
CTGGACCCCT CCAACACCAC CCCCAGAGGG GTGGCCCGGC GCTACGGGGG GGAGTGGACG      1200
GAGGANGCGG GGGAGCGGGC CCTCCTNTCC GAGAGGCTCT TCCNGAACCT NNNGCAGCGC      1260
CTTGAGGGGG AGGAGAGGCT CCTTTGGCTT TACCAGGAGG TGGAGAAGCC CCTTTCCCGG      1320
GTCCTGGCCC ACATGGAGGC CACGGGGGTN CGGCTGGACG TGGCCTACCT CCAGGCCCTN      1380
TCCCTGGAGG TGGCGGAGGA GATCCGCCGC CTCGAGGAGG AGGTCTTCCG CCTGGCCGGC      1440
CACCCCTTCA ACCTCAACTC CCGGGACCAG CTGGAAAGGG TGCTCTTTGA CGAGCTNGGG      1500
CTTCCCGCCA TCGGCAAGAC GGAGAAGACN GGCAAGCGCT CCACCAGCGC CGCCGTGCTG      1560
GAGGCCCTNC GNGAGGCCCA CCCCATCGTG GAGAAGATCC TGCAGTACCG GGAGCTCACC      1620
AAGCTCAAGA ACACCTACAT NGACCCCTG CCNGNCCTCG TCCACCCAG GACGGGCCGC      1680
CTCCACACCC GCTTCAACCA GACGGCCACG GCCACGGGCA GGCTTAGTAG CTCCGACCCC      1740
AACCTGCAGA ACATCCCCGT CCGCACCCCN CTGGGCCAGA GGATCCGCCG GGCCTTCGTG      1800
GCCGAGGAGG GNTGGGTGTT GGTGGCCCTG GACTATAGCC AGATAGAGCT CCGGGTCTTG      1860
GCCACCTCT CCGGGGACGA GAACCTGATC CGGGTCTTCC AGGAGGGGAG GGACATCCAC      1920
ACCCAGACCG CCAGCTGGAT GTTCGGCGTC CCCCCGAGG CCGTGGACCC CCTGATGCGC      1980
CGGGCGGCCA AGACCATCAA CTTCGGGGTC CTCTACGGCA TGTCCGCCCA CCGCCTCTCC      2040
CAGGAGCTTG CCATCCCCTA CGAGGAGGCG GTGGCCTTCA TTGAGCGCTA CTTCCAGAGC      2100
TTCCCAAGG TGCGGGCCTG GATTGAGAAG ACCCTGGAGG AGGGCAGGAG GCGGGGGTAC      2160
GTGGAGACCC TCTTCGGCCG CCGGCGCTAC GTGCCCAGACC TCAACGCCCG GGTGAAGAGC      2220
GTGCGGGAGG CGGCGGAGCG CATGGCCTTC AACATGCCCC TCCAGGGCAC CGCCGCCGAC      2280
CTCATGAAGC TGGCCATGGT GAAGCTCTTC CCCC GGCTNC AGGAAATGGG GGCCAGGATG      2340
CTCCTNCAGG TCCACGACGA GCTGGTCCTC GAGGCCCCCA AAGAGCGGGC GGAGGNGGTG      2400
GCCGCTTTGG CCAAGGAGGT CATGGAGGGG GTCTATCCCC TGGCCGTGCC CCTGGAGGTG      2460
GAGGTGGGGA TGGGGGAGGA CTGGCTCTCC GCCAAGGAGT AG                          2502

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(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 833 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

Variable	Mean	SD	Min	Max
Age	34.5	10.5	18	65
Gender	0.5	0.5	0	1
Marital status	0.5	0.5	0	1
Education	12.5	1.5	9	16
Income	1.5	0.5	1	2
Health status	1.5	0.5	1	2
Stress level	1.5	0.5	1	2
Life satisfaction	1.5	0.5	1	2
Work satisfaction	1.5	0.5	1	2
Family satisfaction	1.5	0.5	1	2
Community satisfaction	1.5	0.5	1	2
Overall satisfaction	1.5	0.5	1	2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met 1	Xaa	Ala	Met	Leu 5	Pro	Leu	Phe	Glu	Pro 10	Lys	Gly	Arg	Val	Leu 15	Leu
Val	Asp	Gly	His 20	His	Leu	Ala	Tyr	Arg 25	Thr	Phe	Phe	Ala	Leu 30	Lys	Gly
Leu	Thr	Thr	Ser 35	Arg	Gly	Glu	Pro 40	Val	Gln	Ala	Val	Tyr 45	Gly	Phe	Ala
Lys	Ser 50	Leu	Leu	Lys	Ala	Leu 55	Lys	Glu	Asp	Gly	Asp 60	Ala	Val	Xaa	Val
Val 65	Phe	Asp	Ala	Lys	Ala 70	Pro	Ser	Phe	Arg	His 75	Glu	Ala	Tyr	Glu	Ala 80
Tyr	Lys	Ala	Gly	Arg 85	Ala	Pro	Thr	Pro	Glu 90	Asp	Phe	Pro	Arg	Gln 95	Leu
Ala	Leu	Ile	Lys 100	Glu	Leu	Val	Asp	Leu 105	Leu	Gly	Leu	Xaa	Arg 110	Leu	Glu
Val	Pro	Gly 115	Tyr	Glu	Ala	Asp	Asp 120	Val	Leu	Ala	Thr	Leu 125	Ala	Lys	Lys
Ala	Glu 130	Lys	Glu	Gly	Tyr	Glu 135	Val	Arg	Ile	Leu	Thr 140	Ala	Asp	Arg	Asp
Leu 145	Tyr	Gln	Leu	Leu	Ser 150	Asp	Arg	Ile	Ala	Val 155	Leu	His	Pro	Glu	Gly 160
Tyr	Leu	Ile	Thr	Pro 165	Ala	Trp	Leu	Trp	Glu 170	Lys	Tyr	Gly	Leu	Arg 175	Pro
Glu	Gln	Trp	Val 180	Asp	Tyr	Arg	Ala	Leu 185	Xaa	Gly	Asp	Pro	Ser 190	Asp	Asn
Leu	Pro	Gly 195	Val	Lys	Gly	Ile	Gly 200	Glu	Lys	Thr	Ala	Xaa 205	Lys	Leu	Leu
Xaa	Glu 210	Trp	Gly	Ser	Leu	Glu 215	Asn	Leu	Leu	Lys	Asn 220	Leu	Asp	Arg	Val
Lys 225	Pro	Xaa	Xaa	Arg	Glu 230	Lys	Ile	Xaa	Ala	His 235	Met	Glu	Asp	Leu	Xaa 240
Leu	Ser	Xaa	Xaa	Leu 245	Ser	Xaa	Val	Arg	Thr 250	Asp	Leu	Pro	Leu	Glu 255	Val
Asp	Phe	Ala	Xaa 260	Arg	Arg	Glu	Pro	Asp 265	Arg	Glu	Gly	Leu	Arg 270	Ala	Phe
Leu	Glu	Arg 275	Leu	Glu	Phe	Gly	Ser 280	Leu	Leu	His	Glu	Phe 285	Gly	Leu	Leu
Glu	Xaa 290	Pro	Lys	Ala	Leu	Glu 295	Glu	Ala	Pro	Trp	Pro 300	Pro	Pro	Glu	Gly

Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala	Glu	305	310	315	320
Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Xaa	Gly	Arg	Val	His	Arg	Ala	Xaa		325	330	335
Asp	Pro	Leu	Xaa	Gly	Leu	Arg	Asp	Leu	Lys	Glu	Val	Arg	Gly	Leu	Leu	340	345	350	
Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Asp	Leu	Xaa	355	360	365	
Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	Asn	370	375	380	
Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	Glu	385	390	395	400
Asp	Ala	Gly	Glu	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	Phe	Xaa	Asn	Leu		405	410	415
Xaa	Xaa	Arg	Leu	Glu	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Xaa	Glu		420	425	430
Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	Glu	Ala	Thr	Gly	435	440	445	
Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser	Leu	Glu	Val	Ala	450	455	460	
Glu	Glu	Ile	Arg	Arg	Leu	Glu	Glu	Glu	Val	Phe	Arg	Leu	Ala	Gly	His	465	470	475	480
Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	Asp		485	490	495
Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	Arg		500	505	510
Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	Ile	515	520	525	
Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Asn	Thr	530	535	540	
Tyr	Ile	Asp	Pro	Leu	Pro	Xaa	Leu	Val	His	Pro	Arg	Thr	Gly	Arg	Leu	545	550	555	560
His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser		565	570	575
Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln	580	585	590	
Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Glu	Gly	Trp	Xaa	Leu	Val	Ala	595	600	605	
Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly	610	615	620	
Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	Thr	625	630	635	640

GACCTCCTGG	CCAGCCTGGC	CAAGAAGGCG	GAAAAGGAGG	GCTACGAGGT	CCGCATCCTC	420
ACCGCCGACA	AAGACCTTTA	CCAGCTCCTT	TCCGACCGCA	TCCACGTCCT	CCACCCCGAG	480
GGGTACCTCA	TCACCCCGGC	CTGGCTTTGG	GAAAAGTACG	GCCTGAGGCC	CGACCAGTGG	540
GCCGACTACC	GGGCCCTGAC	CGGGGACGAG	TCCGACAACC	TTCCCGGGGT	CAAGGGCATC	600
GGGGAGAAGA	CGGCGAGGAA	GCTTCTGGAG	GAGTGGGGGA	GCCTGGAAGC	CCTCCTCAAG	660
AACCTGGACC	GGCTGAAGCC	CGCCATCCGG	GAGAAGATCC	TGGCCACAT	GGACGATCTG	720
AAGCTCTCCT	GGGACCTGGC	CAAGGTGCGC	ACCGACCTGC	CCCTGGAGGT	GGACTTCGCC	780
AAAAGGCGGG	AGCCCAGCCG	GGAGAGGCTT	AGGGCCTTTC	TGGAGAGGCT	TGAGTTTGGC	840
AGCCTCCTCC	ACGAGTTCGG	CCTTCTGGAA	AGCCCCAAGG	CCCTGGAGGA	GGCCCCCTGG	900
CCCCCGCCGG	AAGGGGCCTT	CGTGGGCTTT	GTGCTTTCCC	GCAAGGAGCC	CATGTGGGCC	960
GATCTTCTGG	CCCTGGCCGC	CGCCAGGGGG	GGCCGGGTCC	ACCGGGCCCC	CGAGCCTTAT	1020
AAAGCCCTCA	GGGACCTGAA	GGAGGCGCGG	GGGCTTCTCG	CCAAAGACCT	GAGCGTTCTG	1080
GCCCTGAGGG	AAGGCCTTGG	CCTCCCGCCC	GGCGACGACC	CCATGCTCCT	CGCCTACCTC	1140
CTGGACCCTT	CCAACACCAC	CCCCGAGGGG	GTGGCCCGGC	GCTACGGCGG	GGAGTGGACG	1200
GAGGAGGCGG	GGGAGCGGGC	CGCCCTTTCC	GAGAGGCTCT	TCGCCAACCT	GTGGGGGAGG	1260
CTTGAGGGGG	AGGAGAGGCT	CCTTTGGCTT	TACCGGGAGG	TGGAGAGGCC	CCTTTCGGCT	1320
GTCTTGCCCC	ACATGGAGGC	CACGGGGGTG	CGCCTGGACG	TGGCCTATCT	CAGGGCCTTG	1380
TCCCTGGAGG	TGGCCGGGGA	GATCGCCCGC	CTCGAGGCCG	AGGTCTTCCG	CCTGGCCGGC	1440
CACCCCTTCA	ACCTCAACTC	CCGGGACCAG	CTGGAAAGGG	TCCTCTTTGA	CGAGCTAGGG	1500
CTTCCCGCCA	TCGGCAAGAC	GGAGAAGACC	GGCAAGCGCT	CCACCAGCGC	CGCCGTCCTG	1560
GAGGCCCTCC	GCGAGGCCCA	CCCCATCGTG	GAGAAGATCC	TGCAGGCATG	CAAGCTTGGC	1620
ACTGGCCGTC	GTTTTACAAC	GTCGTGA				1647

(2) INFORMATION FOR SEQ ID NO:10:

(ii) MOLECULE TYPE: DNA (genomic)

ATGAATTCGG	GGATGCTGCC	CCTCTTTGAG	CCCAAGGGCC	GGGTCTCCT	GGTGGACGGC	60
CACCACCTGG	CCTACCGCAC	CTTCCACGCC	CTGAAGGGCC	TCACCACCAG	CCGGGGGGAG	120
CCGGTGACAG	CGGTCTACGG	CTTCGCCAAG	AGCCTCCTCA	AGGCCCTCAA	GGAGGACGGG	180

GACGCGGTGA	TCGTGGTCTT	TGACGCCAAG	GCCCCCTCCT	TCCGCCACGA	GGCCTACGGG	240
GGGTACAAGG	CGGGCCGGGC	CCCCACGCCG	GAGGACTTTC	CCCGGCAACT	CGCCCTCATC	300
AAGGAGCTGG	TGGACCTCCT	GGGGCTGGCG	CGCCTCGAGG	TCCCGGGCTA	CGAGGCGGAC	360
GACGTCCTGG	CCAGCCTGGC	CAAGAAGGCG	GAAAAGGAGG	GCTACGAGGT	CCGCATCCTC	420
ACCGCCGACA	AAGACCTTTA	CCAGCTCCTT	TCCGACCGCA	TCCACGTCCT	CCACCCCGAG	480
GGGTACCTCA	TCACCCCGGC	CTGGCTTTTG	GAAAAGTACG	GCCTGAGGCC	CGACCAGTGG	540
GCCGACTACC	GGGCCCTGAC	CGGGGACGAG	TCCGACAAAC	TTCCCGGGGT	CAAGGGCATC	600
GGGGAGAAGA	CGGCGAGGAA	GCTTCTGGAG	GAGTGGGGGA	GCCTGGAAGC	CCTCCTCAAG	660
AACCTGGACC	GGCTGAAGCC	CGCCATCCGG	GAGAAGATCC	TGGCCACAT	GGACGATCTG	720
AAGCTCTCCT	GGGACCTGGC	CAAGGTGCGC	ACCGACCTGC	CCCTGGAGGT	GGACTTCGCC	780
AAAAGGCGGG	AGCCCGACCG	GGAGAGGCTT	AGGGCCTTTC	TGGAGAGGCT	TGAGTTTGGC	840
AGCCTCCTCC	ACGAGTTCGG	CCTTCTGGAA	AGCCCCAAGG	CCCTGGAGGA	GGCCCCCTGG	900
CCCCCGCCGG	AAGGGGCTT	CGTGGGCTTT	GTGCTTTCCC	GCAAGGAGCC	CATGTGGGCC	960
GATCTTCTGG	CCCTGGCCGC	CGCCAGGGGG	GGCCGGGTCC	ACCGGGCCCC	CGAGCCTTAT	1020
AAAGCCCTCA	GGGACCTGAA	GGAGGCGCGG	GGGCTTCTCG	CCAAAGACCT	GAGCGTTCTG	1080
GCCCTGAGGG	AAGGCCTTGG	CCTCCCGCCC	GGCGACGACC	CCATGCTCCT	CGCCTACCTC	1140
CTGGACCCCT	CCAACACCAC	CCCCGAGGGG	GTGGCCCCGC	GCTACGGCGG	GGAGTGGACG	1200
GAGGAGGCGG	GGGAGCGGGC	CGCCCTTTCC	GAGAGGCTCT	TCGCCAACCT	GTGGGGGAGG	1260
CTTGAGGGGG	AGGAGAGGCT	CCTTTGGCTT	TACCGGGAGG	TGGAGAGGCC	CCTTTCCGCT	1320
GTCTTGCCCC	ACATGGAGGC	CACGGGGGTG	CGCCTGGACG	TGGCCTATCT	CAGGGCCTTG	1380
TCCCTGGAGG	TGGCCGGGGA	GATCGCCCCG	CTCGAGGCCG	AGGTCTTCCG	CCTGGCCGGC	1440
CACCCCTTCA	ACCTCAACTC	CCGGGACCAG	CTGGAAAGGG	TCCTCTTTGA	CGAGCTAGGG	1500
CTTCCCGCCA	TCGGCAAGAC	GGAGAAGACC	GGCAAGCGCT	CCACCAGCGC	CGCCGTCCTG	1560
GAGGCCCTCC	GCGAGGCCCA	CCCCATCGTG	GAGAAGATCC	TGCAGTACCG	GGAGCTCACC	1620
AAGCTGAAGA	GCACCTACAT	TGACCCCTTG	CCGGACCTCA	TCCACCCAG	GACGGGCCGC	1680
CTCCACACCC	GCTTCAACCA	GACGGCCACG	GCCACGGGCA	GGCTAAGTAG	CTCCGATCCC	1740
AACCTCCAGA	ACATCCCCGT	CCGCACCCCG	CTTGGGCAGA	GGATCCGCCG	GGCCTTCATC	1800
GCCGAGGAGG	GGTGGCTATT	GGTGGCCCTG	GACTATAGCC	AGATAGAGCT	CAGGGTGCTG	1860
GCCCACCTCT	CCGGCGACGA	GAACCTGATC	CGGGTCTTCC	AGGAGGGGCG	GGACATCCAC	1920
ACGAGACCG	CCAGCTGGAT	GTTCGGCGTC	CCCCGGGAGG	CCGTGGACCC	CCTGATGCGC	1980
CGGGCGGCCA	AGACCATCAA	CTTCGGGGTC	CTCTACGGCA	TGTCGGCCCA	CCGCCTCTCC	2040

CAGGAGCTAG CTAGCCATCC CTTACGAGGA GGCCAGGCC TTCATTGA

2088

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 962 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGAATTCGG GGATGCTGCC CCTCTTTGAG CCCAAGGGCC GGGTCCTCCT GGTGGACGGC 60
CACCACCTGG CCTACCGCAC CTTCCACGCC CTGAAGGGCC TCACCACCAG CCGGGGGGAG 120
CCGGTGCAGG CGGTCTACGG CTTGCGCAAG AGCCTCCTCA AGGCCCTCAA GGAGGACGGG 180
GACGCGGTGA TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGGG 240
GGGTACAAGG CGGGCCGGGC CCCACGCCG GAGGACTTTC CCCGGCAACT CGCCCTCATC 300
AAGGAGCTGG TGGACCTCCT GGGGCTGGCG CGCCTCGAGG TCCCGGGCTA CGAGGCGGAC 360
GACGTCTTGG CCAGCCTGGC CAAGAAGGCG GAAAAGGAGG GCTACGAGGT CCGCATCCTC 420
ACCGCCGACA AAGACCTTTA CCAGCTTCTT TCCGACCGCA TCCACGTCTT CCACCCCGAG 480
GGGTACCTCA TCACCCCGGC CTGGCTTTGG GAAAAGTACG GCCTGAGGCC CGACCAAGTG 540
GCCGACTACC GGGCCCTGAC CGGGGACGAG TCCGACAACC TTCCCGGGGT CAAGGGCATC 600
GGGGAGAAGA CGGCGAGGAA GCTTCTGGAG GAGTGGGGGA GCCTGGAAGC CCTCCTCAAG 660
AACCTGGACC GGCTGAAGCC CGCCATCCGG GAGAAGATCC TGGCCACAT GGACGATCTG 720
AAGCTCTCCT GGGACCTGGC CAAGGTGCGC ACCGACCTGC CCCTGGAGGT GGAATTCGCC 780
AAAAGGCGGG AGCCCGACCG GGAGAGGCTT AGGGCCTTTC TGGAGAGGCT TGAGTTTGGC 840
AGCCTCCTCC ACGAGTTCGG CTTCTGGAA AGCCCCAAGT CATGGAGGGG GTGTATCCCC 900
TGGCCGTGCC CCTGGAGGTG GAGGTGGGGA TAGGGGAGGA CTGGCTCTCC GCCAAGGAGT 960
GA 962

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1600 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGAATTCG GGGATGCTGC CCCTCTTGA GCCCAAGGGC CGGGTCCTCC TGGTGGACGG 60

CCACCACCTG GCCTACCGCA CCTTCCACGC CCTGAAGGGC CTCACCACCA GCCGGGGGGA	120
GCCGGTGCAG GCGGTCTACG GCTTCGCCAA GAGCCTCCTC AAGGCCCTCA AGGAGGACGG	180
GGACGCGGTG ATCGTGGTCT TTGACGCCAA GGCCCCCTCC TTCCGCCACG AGGCCTACGG	240
GGGGTACAAG GCGGGCCGGG CCCCCACGCC GGAGGACTTT CCCC GGCAAC TCGCCCTCAT	300
CAAGGAGCTG GTGGACCTCC TGGGGCTGGC GCGCCTCGAG GTCCCGGGCT ACGAGGCGGA	360
CGACGTCCTG GCCAGCCTGG CCAAGAAGGC GGAAAAGGAG GGCTACGAGG TCCGCATCCT	420
CACCGCCGAC AAAGACCTTT ACCAGCTCCT TTCCGACCGC ATCCACGTCC TCCACCCCGA	480
GGGGTACCTC ATCACCCCGG CCTGGCTTTG GGAAAAGTAC GGCCTGAGGC CCGACCACTG	540
GGCCGACTAC CGGGCCCTGA CCGGGGACGA GTCCGACAAC CTTCCCGGGG TCAAGGGCAT	600
CGGGGAGAAG ACGGCGAGGA AGCTTCTGGA GGAGTGGGGG AGCCTGGAAG CCCTCCTCAA	660
GAACCTGGAC CGGCTGAAGC CCGCCATCCG GGAGAAGATC CTGGCCCACA TGGACGATCT	720
GAAGCTCTCC TGGGACCTGG CCAAGGTGCG CACCGACCTG CCCCTGGAGG TGGACTTCGC	780
CAAAAGGCGG GAGCCCGACC GGGAGAGGCT TAGGGCCTTT CTGGAGAGGC TTGAGTTTGG	840
CAGCCTCCTC CACGAGTTCG GCCTTCTGGA AAGCCCCAAG ATCCGCCGGG CCTTCATCGC	900
CGAGGAGGGG TGGCTATTGG TGGCCCTGGA CTATAGCCAG ATAGAGCTCA GGGTGCTGGC	960
CCACCTCTCC GGCACGAGA ACCTGATCCG GGTCTTCCAG GAGGGGCGGG ACATCCACAC	1020
GGAGACCGCC AGCTGGATGT TCGGCGTCCC CCGGGAGGCC GTGGACCCCC TGATGCGCCG	1080
GGCGGCCAAG ACCATCAACT TCGGGGTCCT CTACGGCATG TCGGCCACC GCCTCTCCCA	1140
GGAGCTAGCC ATCCCTTACG AGGAGGCCCA GGCCTTCATT GAGCGCTACT TTCAGAGCTT	1200
CCCCAAGGTG CGGGCCTGGA TTGAGAAGAC CCTGGAGGAG GGCAGGAGGC GGGGGTACGT	1260
GGAGACCCTC TTCGGCCGCC GCCGCTACGT GCCAGACCTA GAGGCCCGGG TGAAGAGCGT	1320
GCGGGAGGCG GCCGAGCGCA TGGCCTTCAA CATGCCCGTC CGGGGCACCG CCGCCGACCT	1380
CATGAAGCTG GCTATGGTGA AGCTCTTCCC CAGGCTGGAG GAAATGGGG CCAGGATGCT	1440
CCTTCAGGTC CACGACGAGC TGGTCTCTGA GGCCCCAAAA GAGAGGGCGG AGGCCGTGGC	1500
CCGGCTGGCC AAGGAGGTCA TGGAGGGGGT GTATCCCCTG GCCGTGCCCC TGGAGGTGGA	1560
GGTGGGGATA GGGGAGGACT GGCTCTCCGC CAAGGAGTGA	1600

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

[illegible]

36

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

34

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 91 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

60

91

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

20

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

27

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTAATCATGG TCATAGCTGG TAGCTTGCTA C

31

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGATCCTCTA GAGTCGACCT GCAGGCATGC CTACCTTGGT AG

42

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGATCCTCTA GAGTCGACCT GCAGGCATGC

30

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2502 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATGAATTCGG GGATGCTGCC CCTCTTTGAG CCCAAGGGCC GGGTCCTCCT GGTGGACGGC

60

CACCACCTGG CCTACGCAC CTTCCACGCC CTGAAGGGCC TCACCACCAG CCGGGGGGAG

120

CCGGTGCAGG CGGTCTACGG CTTCCGCAAG AGCCTCCTCA AGGCCCTCAA GGAGGACGGG

180

GACGCGGTGA TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGGG

240

GGGTACAAGG CGGGCCGGGC CCCACGCCG GAGGACTTTC CCCGGCAACT CGCCCTCATC	300
AAGGAGCTGG TGGACCTCCT GGGGCTGGCG CGCCTCGAGG TCCCGGGCTA CGAGGCGGAC	360
GACGTCCTGG CCAGCCTGGC CAAGAAGGCG GAAAAGGAGG GCTACGAGGT CCGCATCCTC	420
ACCGCCGACA AAGACCTTTA CCAGCTCCTT TCCGACCGCA TCCACGTCCT CCACCCCGAG	480
GGGTACCTCA TCACCCCGGC CTGGCTTTGG GAAAAGTACG GCCTGAGGCC CGACCAGTGG	540
GCCGACTACC GGGCCCTGAC CGGGGACGAG TCCGACAACC TTCCCGGGGT CAAGGGCATC	600
GGGGAGAAGA CGGCGAGGAA GCTTCTGGAG GAGTGGGGGA GCCTGGAAGC CCTCCTCAAG	660
AACCTGGACC GGCTGAAGCC CGCCATCCGG GAGAAGATCC TGGCCACAT GGACGATCTG	720
AAGCTCTCCT GGGACCTGGC CAAGGTGCGC ACCGACCTGC CCCTGGAGGT GGA CTTCGCC	780
AAAAGGCGGG AGCCCGACCG GGAGAGGCTT AGGGCCTTTC TGGAGAGGCT TGAGTTTGGC	840
AGCCTCCTCC ACGAGTTCGG CTTTCTGGAA AGCCCCAAGG CCCTGGAGGA GGCCCCCTGG	900
CCCCGCCCGG AAGGGGCCTT CGTGGGCTTT GTGCTTTCCC GCAAGGAGCC CATGTGGGCC	960
GATCTTCTGG CCCTGGCCGC CGCCAGGGGG GGCCGGGTCC ACCGGGCCCC CGAGCCTTAT	1020
AAAGCCCTCA GGGACCTGAA GGAGGCGCGG GGGCTTCTCG CCAAAGACCT GAGCGTTCTG	1080
GCCCTGAGGG AAGGCCTTGG CCTCCCGCCC GGCGACGACC CCATGCTCCT CGCCTACCTC	1140
CTGGACCCTT CCAACACCAC CCCCAGGGGG GTGGCCCGGC GCTACGGCGG GGAGTGGACG	1200
GAGGAGGCGG GGGAGCGGGC CGCCCTTTCC GAGAGGCTCT TCGCCAACCT GTGGGGGAGG	1260
CTTGAGGGGG AGGAGAGGCT CCTTTGGCTT TACCGGGAGG TGGAGAGGCC CCTTTCGCT	1320
GTCCTGGCCC ACATGGAGGC CACGGGGGTG CGCCTGGACG TGGCCTATCT CAGGGCCTTG	1380
TCCCTGGAGG TGCCCGGGGA GATCGCCCGC CTCGAGGCCG AGGTCTTCCG CCTGGCCGGC	1440
CACCCCTTCA ACCTCAACTC CCGGGACCAG CTGGAAAGGG TCCTCTTTGA CGAGCTAGGG	1500
CTTCCCGCCA TCGGCAAGAC GGAGAAGACC GGCAAGCGCT CCACCAGCGC CGCCGTCCTG	1560
GAGGCCCTCC GCGAGGCCCA CCCATCGTG GAGAAGATCC TGCAGTACCG GGAGCTCACC	1620
AAGCTGAAGA GCACCTACAT TGACCCCTTG CCGGACCTCA TCCACCCAG GACGGGCCGC	1680
CTCCACACCC GCTTCAACCA GACGGCCACG GCCACGGGCA GGCTAAGTAG CTCCGATCCC	1740
AACCTCCAGA ACATCCCCGT CCGCACCCCG CTTGGGCAGA GGATCCGCCG GGCCTTCATC	1800
GCCGAGGAGG GGTGGCTATT GGTGGCCCTG GACTATAGCC AGATAGAGCT CAGGGTGCTG	1860
GCCCACCTCT CCGGCGACGA GAACCTGATC CGGGTCTTCC AGGAGGGGCG GGACATCCAC	1920
ACGGAGACCG CCAGCTGGAT GTTCGGCGTC CCCCAGGAGG CCGTGGACCC CCTGATGCGC	1980
CGGGCGGCCA AGACCATCAA CTTCGGGGTC CTCTACGGCA TGTCGGCCCA CCGCTCTCC	2040
CAGGAGCTAG CCATCCCTTA CGAGGAGGCC CAGGCCTTCA TTGAGCGCTA CTTTCAGAGC	2100

TTCCCCAAGG TGCGGGCCTG GATTGAGAAG ACCCTGGAGG AGGGCAGGAG GCGGGGGTAC 2160
 GTGGAGACCC TCTTCGGCCG CCGCCGCTAC GTGCCAGACC TAGAGGCCCG GGTGAAGAGC 2220
 GTGCGGGAGG CGGCCGAGCG CATGGCCTTC AACATGCCCC TCCGGGGCAC CGCCGCCGAC 2280
 CTCATGAAGC TGGCTATGGT GAAGCTCTTC CCCAGGCTGG AGGAAATGGG GGCCAGGATG 2340
 CTCCTTCAGG TCCACGACGA GCTGGTCCTC GAGGCCCCAA AAGAGAGGGC GGAGGCCGTG 2400
 GCCCCGGCTGG CCAAGGAGGT CATGGAGGGG GTGTATCCCC TGGCCGTGCC CCTGGAGGTG 2460
 GAGGTGGGGA TAGGGGAGGA CTGGCTCTCC GCCAAGGAGT GA 2502

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GATTTAGGTG AACTATAG 19

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CGGACGAACA AGCGAGACAG CGACACAGGT ACCACATGGT ACAAGAGGCA AGAGAGACGA 60
 CACAGCAGAA AC 72

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTTTCTGCTG TGTCGTCTCT CTTGCCTCTT GTACCATGTG GTACCTGTGT CGCTGTCTCG 60
 CTTGTTCGTC 70

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GACGAACAAG CGAGACAGCG

20

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTTTCTGCTG TGTCGTCTCT CTTG

24

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCTCTTGCTAC CATGTGGTAC CTGTGTCGCT GTCTCGCTTG TTCGTC

46

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ACACAGGTAC CACATGGTAC AAGAGGCAAG AGAGACGACA CAGCAGAAAC

50

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met	Ala	Ser	Met	Thr	Gly	Gly	Gln	Gln	Met	Gly	Arg	Ile	Asn	Ser
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 969 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATGGCTAGCA TGACTGGTGG ACAGCAAATG GGTCGGATCA ATTCGGGGAT GCTGCCCCCTC 60
TTTGAGCCCA AGGGCCGGGT CCTCCTGGTG GACGGCCACC ACCTGGCCTA CCGCACCTTC 120
CACGCCCTGA AGGGCCTCAC CACCAGCCGG GGGGAGCCGG TGCAGGCGGT CTACGGCTTC 180
GCCAAGAGCC TCCTCAAGGC CCTCAAGGAG GACGGGGACG CGGTGATCGT GGTCTTTGAC 240
GCCAAGGCCC CCTCCTTCCG CCACGAGGCC TACGGGGGGT ACAAGGCGGG CCGGGCCCCC 300
ACGCCGGAGG ACTTTCCCCG GCAACTCGCC CTCATCAAGG AGCTGGTGGA CCTCCTGGGG 360
CTGGCGCGCC TCGAGGTCCC GGGCTACGAG GCGGACGACG TCCTGGCCAG CCTGGCCAAG 420
AAGGCGGAAA AGGAGGGCTA CGAGGTCCGC ATCCTCACCG CCGACAAAGA CCTTTACCAG 480
CTTCTTTCCG ACCGCATCCA CGTCCTCCAC CCCGAGGGGT ACCTCATCAC CCCGGCCTGG 540
CTTTGGGAAA AGTACGGCCT GAGGCCCGAC CAGTGGGCCG ACTACCGGGC CCTGACCGGG 600
GACGAGTCCG ACAACCTTCC CGGGGTCAAG GGCATCGGGG AGAAGACGGC GAGGAAGCTT 660
CTGGAGGAGT GGGGGAGCCT GGAAGCCCTC CTCAAGAACC TGGACCGGCT GAAGCCCGCC 720
ATCCGGGAGA AGATCCTGGC CCACATGGAC GATCTGAAGC TCTCCTGGGA CCTGGCCAAG 780
GTGCGCACCG ACCTGCCCCT GGAGGTGGAC TTCGCCAAA GGCGGGAGCC CGACCGGGAG 840
AGGCTTAGGG CCTTTCTGGA GAGGCTTGAG TTTGGCAGCC TCCTCCACGA GTTCGGCCTT 900
CTGGAAAGCC CCAAGTCATG GAGGGGGTGT ATCCCCTGGC CGTGCCCCTG GAGGTGGAGG 960
TGGGGATAG 969

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 948 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGGCTAGCA TGACTGGTGG ACAGCAAATG GGTCGGATCA ATTCGGGGAT GCTGCCCCCTC	60
TTTGAGCCCA AGGGCCGGGT CCTCCTGGTG GACGGCCACC ACCTGGCCTA CCGCACCTTC	120
CACGCCCTGA AGGGCCTCAC CACCAGCCGG GGGGAGCCGG TGCAGGCGGT CTACGGCTTC	180
GCCAAGAGCC TCCTCAAGGC CCTCAAGGAG GACGGGGACG CGGTGATCGT GGTCTTTGAC	240
GCCAAGGCCC CCTCCTTCCG CCACGAGGCC TACGGGGGGT ACAAGGCGGG CCGGGCCCCC	300
ACGCCGGAGG ACTTTCCCCG GCAACTCGCC CTCATCAAGG AGCTGGTGGA CCTCCTGGGG	360
CTGGCGCGCC TCGAGGTCCC GGGCTACGAG GCGGACGACG TCCTGGCCAG CCTGGCCAAG	420
AAGGCGGAAA AGGAGGGCTA CGAGGTCCGC ATCCTCACC GCGACAAAGA CCTTTACCAG	480
CTTCTTTCCG ACCGCATCCA CGTCCTCCAC CCCGAGGGGT ACCTCATCAC CCCGGCCTGG	540
CTTTGGGAAA AGTACGGCCT GAGGCCCGAC CAGTGGGCCG ACTACCGGGC CCTGACCGGG	600
GACGAGTCCG ACAACCTTCC CGGGGTCAAG GGCATCGGGG AGAAGACGGC GAGGAAGCTT	660
CTGGAGGAGT GGGGGAGCCT GGAAGCCCTC CTCAAGAACC TGGACCGGCT GAAGCCCGCC	720
ATCCGGGAGA AGATCCTGGC CCACATGGAC GATCTGAAGC TCTCCTGGGA CCTGGCCAAG	780
GTGCGCACCG ACCTGCCCCT GGAGGTGGAC TTCGCCAAA GGCGGGAGCC CGACCGGGAG	840
AGGCTTAGGG CCTTTCTGGA GAGGCTTGAG TTTGGCAGCC TCCTCCACGA GTTCGGCCTT	900
CTGGAAAGCC CCAAGGCCGC ACTCGAGCAC CACCACCACC ACCACTGA	948

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 206 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGCCAGGGTT TTCCAGTCA CGACGTTGTA AAACGACGGC CAGTGAATTG TAATACGACT	60
CACTATAGGG CGAATTCGAG CTCGGTACCC GGGGATCCTC TAGAGTCGAC CTGCAGGCAT	120
GCAAGCTTGA GTATTCTATA GTGTCACCTA AATAGCTTGG CGTAATCATG GTCATAGCTG	180
TTTCCTGTGT GAAATTGTTA TCCGCT	206

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TTCTGGGTTC TCTGCTCTCT GGTCGCTGTC TCGCTTGTTTC GTC

43

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCTGTCTCGC TTGTTTCGTC

19

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GACGAACAAG CGAGACAGCG

20

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTCTGGGTTC TCTGCTCTCT GGTC

24

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GACGAACAAG CGAGACAGCG ACCAGAGAGC AGAGAACCCA GAA

43

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ACCAGAGAGC AGAGAACCCA GAA

23

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AACAGCTATG ACCATGATTA C

21

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCGGGAA

60

TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA

120

GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAG

157

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTAGACA TAACCGGGAA

60

TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA

120

157

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

19

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

60

120

180

240

300

339

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GCCTTATTTT ACTTTAAAAA T

21

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TAAAGTTTTG TGTATCTCA

20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCGGGAA

60

TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA

120

GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAG

157

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTGAATCTTG TAGATAGCTA TAGTCATAGC CCAGATCTTT GGATGAAATA AAGAAATCAC

60

CATTTCTGTA CAGTGGTATA AAAGGAACCA TGTAGGATTC CCGGTTATGT CCAATGGGTG

120

CATTGGCTTC TGGATAAACT TCTTGAAGAG GACGGTG

157

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AGCGGATAAC AATTTACAC AGGAAACAGC TATGACCATG ATTACGCCAA GCTATTAGG 60
TGACACTATA GAATACTCAA GCTTGCATGC CTGCAGGTCG ACTCTAGAGG ATCCCCGGGT 120
ACCGAGCTCG AATTCGCCCT ATAGTGAGTC GTATTAGGAT CCGTG 165

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CGCCAGGGTT TTCCAGTCA CGACGTTGTA AAACGACGGC CAGTGAATTG TAATACGACT 60
CACTATAGGG CGAATTCGAG CTCGGTACCC GGGGATCCTC TAGAGTCGAC CTGCAGGCAT 120
GCAAGCTTGA GTATTCTATA GTGTCACCTA AATAGCTTGG CGTAATCATG GTCATAGCTG 180
TTTCCTGTGT GAAATTGTTA TCCGCT 206

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AGCGGATAAC AATTTACAC AGGA 24

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CACGGATCCT AATACGACTC ACTATAGGG 29

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CGCCAGGGTT TTCCAGTCA CGAC

24

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTAGACA TAACCGGGAA

60

TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA

120

GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAG

157

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCAGGAA

60

TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA

120

GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAG

157

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCGGGAA

60

TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA 120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTGAGACC CAGACTCTTT TCAAGACTAC 180
ATTAAGTCCT ATTTGGAACA AGCGAGTCGG ATCTGGTCAT GGCTCCTTGG GCGGCGGATG 240
GTAGGGGCGG TCCTCACTGC CCTGCTGGCA GGGCTTGTGA GCTTGCTGTG TCGTCACAAG 300
AGAAAGCAGC TTCCTGAAGA AAAGCAGCCA CTCCTCATGG AGAAAGAGGA TTACCACAGC 360
TTGTATCAGA GCCATTTA 378

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCAGGAA 60
TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA 120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTGAGACC CAGACTCTTT TCAAGACTAC 180
ATTAAGTCCT ATTTGGAACA AGCGAGTCGG ATCTGGTCAT GGCTCCTTGG GCGGCGGATG 240
GTAGGGGCGG TCCTCACTGC CCTGCTGGCA GGGCTTGTGA GCTTGCTGTG TCGTCACAAG 300
AGAAAGCAGC TTCCTGAAGA AAAGCAGCCA CTCCTCATGG AGAAAGAGGA TTACCACAGC 360
TTGTATCAGA GCCATTTA 378

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1059 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GCAAGTTTGG CTTTTGGGGA CCAAACGCA CAGAGAGACG ACTCTTGGTG AGAAGAAACA 60
TCTTCGATTT GAGTGCCCCA GAGAAGGACA AATTTTTTGC CTACCTCACT TTAGCAAAGC 120
ATACCATCAG CTCAGACTAT GTCATCCCCA TAGGGACCTA TGGCCAAATG AAAAATGGAT 180
CAACACCCAT GTTTAACGAC ATCAATATTT ATGACCTCTT TGTCTGGATG CATTATTATG 240
TGTCAATGGA TGCACTGCTT GGGGGATATG AAATCTGGAG AGACATTGAT TTTGCCCATG 300
AAGCACCAGC TTTTCTGCCT TGGCATAGAC TCTTCTGTG GCGGTGGGAA CAAGAAATCC 360

AGAAGCTGAC	AGGAGATGAA	AAC TTCACTA	TTCCATATTG	GGACTGGCGG	GATGCAGAAA	420
AGTGTGACAT	TTGCACAGAT	GAGTACATGG	GAGGTCAGCA	CCCCACAAAT	CCTAACTTAC	480
TCAGCCCAGC	ATCATTCTTC	TCCTCTTGGC	AGATTGTCTG	TAGCCGATTG	GAGGAGTACA	540
ACAGCCATCA	GTCTTTATGC	AATGGAACGC	CCGAGGGACC	TTTACGGCGT	AATCCTGGAA	600
ACCATGACAA	ATCCAGAACC	CCAAGGCTCC	CCTCTTCAGC	TGATGTAGAA	TTTTGCCTGA	660
GTTTGACCCA	ATATGAATCT	GGTTCCATGG	ATAAAGCTGC	CAATTT CAGC	TTTAGAAATA	720
CACTGGAAGG	ATTTGCTAGT	CCACTTACTG	GGATAGCGGA	TGCCCTCTCA	AGCAGCATGC	780
ACAATGCCTT	GCACATCTAT	ATGAATGGAA	CAATGTCCCA	GGTACAGGGA	TCTGCCAACG	840
ATCCTATCTT	CCTTCTTCAC	CATGCATTTG	TTGACAGTAT	TTTTGAGCAG	TGGCTCCGAA	900
GGCACCCTCC	TCTTCAAGAA	GTTTATCCAG	AAGCCAATGC	ACCCATTGGA	CATAACCGGG	960
AATCCTACAT	GGTTCCTTTT	ATACCACTGT	ACAGAAATGG	TGATTTCTTT	ATTCATCCA	1020
AAGATCTGGG	CTATGACTAT	AGCTATCTAC	AAGATT CAG			1059

(2) INFORMATION FOR SEO ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1059 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GCAAGTTTGG	CTTTTGGGGA	CCAAACTGCA	CAGAGAGACG	ACTCTTGGTG	AGAAGAAACA	60
TCTTCGATTT	GAGTGCCCCA	GAGAAGGACA	AATTTTTTGC	CTACCTCACT	TTAGCAAAGC	120
ATACCATCAG	CTCAGACTAT	GTCATCCCCA	TAGGGACCTA	TGGCCAAATG	AAAAATGGAT	180
CAACACCCAT	GTTTAACGAC	ATCAATATTT	ATGACCTCTT	TGTCTGGATG	CATTATTATG	240
TGTCAATGGA	TGCACTGCTT	GGGGGATATG	AAATCTGGAG	AGACATTGAT	TTTGCCCATG	300
AAGCACCAGC	TTTTCTGCCT	TGGCATAGAC	TCTTCTTGTT	GCGGTGGGAA	CAAGAAATCC	360
AGAAGCTGAC	AGGAGATGAA	AACTTCACTA	TTCCATATTG	GGACTGGCGG	GATGCAGAAA	420
AGTGTGACAT	TTGCACAGAT	GAGTACATGG	GAGGTCAGCA	CCCCACAAAT	CCTAACTTAC	480
TCAGCCCAGC	ATCATTCCTC	TCCTCTTGGC	AGATTGTCTG	TAGCCGATTG	GAGGAGTACA	540
ACAGCCATCA	GTCTTTATGC	AATGGAACGC	CCGAGGGACC	TTTACGGCGT	AATCCTGGAA	600
ACCATGACAA	ATCCAGAACC	CCAAGGCTCC	CCTCTTCAGC	TGATGTAGAA	TTTTGCCTGA	660
GTTTGACCCA	ATATGAATCT	GGTTCATGG	ATAAAGCTGC	CAATTTTCAGC	TTTAGAAATA	720
CACTGGAAGG	ATTTGCTAGT	CCACTTACTG	GGATAGCGGA	TGCCTCTCAA	AGCAGCATGC	780

ACAAATGCCTT	GCACATCTAT	ATGAATGGAA	CAATGTCCCA	GGTACAGGGA	TCTGCCAACG	840
ATCCTATCTT	CCTTCTTCAC	CATGCATTTG	TTGACAGTAT	TTTTGAGCAG	TGGCTCCGAA	900
GGCACCGTCC	TCTTCAAGAA	GTTTATCCAG	AAGCCAATGC	ACCCATTGGA	CATAACCAGG	960
AATCCTACAT	GGTTCCTTTT	ATACCACTGT	ACAGAAATGG	TGATTTCTTT	ATTTTCATCCA	1020
AAGATCTGGG	CTATGACTAT	AGCTATCTAC	AAGATTTCAG			1059

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1587 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATGCTCCTGG	CTGTTTGTGA	CTGCCTGCTG	TGGAGTTTCC	AGACCTCCGC	TGGCCATTTTC	60
CCTAGAGCCT	GTGTCTCCTC	TAAGAACCTG	ATGGAGAAGG	AATGCTGTCC	ACCGTGGAGC	120
GGGGACAGGA	GTCCCTGTGG	CCAGCTTTCA	GGCAGAGGTT	CCTGTCAGAA	TATCCTTCTG	180
TCCAATGCAC	CACTTGGGCC	TCAATTTCCC	TTCACAGGGG	TGGATGACCG	GGAGTCGTGG	240
CCTTCCGTCT	TTTATAATAG	GACCTGCCAG	TGCTCTGGCA	ACTTCATGGG	ATTCAACTGT	300
GGAAACTGCA	AGTTTGGCTT	TTGGGGACCA	AACTGCACAG	AGAGACGACT	CTTGGTGAGA	360
AGAAACATCT	TCGATTTGAG	TGCCCCAGAG	AAGGACAAAT	TTTTTGCCTA	CCTCACTTTA	420
GCAAAGCATA	CCATCAGCTC	AGACTATGTC	ATCCCCATAG	GGACCTATGG	CCAAATGAAA	480
AATGGATCAA	CACCCATGTT	TAACGACATC	AATATTTATG	ACCTCTTTGT	CTGGATGCAT	540
TATTATGTGT	CAATGGATGC	ACTGCTTGGG	GGATATGAAA	TCTGGAGAGA	CATTGATTTT	600
GCCCATGAAG	CACCAGCTTT	TCTGCCTTGG	CATAGACTCT	TCTTGTTGCG	GTGGGAACAA	660
GAAATCCAGA	AGCTGACAGG	AGATGAAAAC	TTCACTATTC	CATATTGGGA	CTGGCGGGAT	720
GCAGAAAAGT	GTGACATTTG	CACAGATGAG	TACATGGGAG	GTCAGCACCC	CACAAATCCT	780
AACTTACTCA	GCCCAGCATC	ATTCTTCTCC	TCTTGGCAGA	TTGTCTGTAG	CCGATTGGAG	840
GAGTACAACA	GCCATCAGTC	TTTATGCAAT	GGAACGCCCG	AGGGACCTTT	ACGGCGTAAT	900
CCTGGAAACC	ATGACAAATC	CAGAACCCCA	AGGCTCCCCT	CTTCAGCTGA	TGTAGAATTT	960
TGCCTGAGTT	TGACCCAATA	TGAATCTGGT	TCCATGGATA	AAGCTGCCAA	TTTCAGCTTT	1020
AGAAATACAC	TGGAAGGATT	TGCTAGTCCA	CTTACTGGGA	TAGCGGATGC	CTCTCAAAGC	1080
AGCATGCACA	ATGCCTTGCA	CATCTATATG	AATGGAACAA	TGTCCCAGGT	ACAGGGATCT	1140
GCCAACGATC	CTATCTTCCT	TCTTCACCAT	GCATTTGTTG	ACAGTATTTT	TGAGCAGTGG	1200

CTCCGAAGGC ACCGTCCTCT TCAAGAAGTT TATCCAGAAG CCAATGCACC CATTGGACAT	1260
AACCGGGAAT CCTACATGGT TCCTTTTATA CCACTGTACA GAAATGGTGA TTTCTTTATT	1320
TCATCCAAAG ATCTGGGCTA TGACTATAGC TATCTACAAG ATTCAGACCC AGACTCTTTT	1380
CAAGACTACA TTAAGTCCTA TTTGGAACAA GCGAGTCGGA TCTGGTCATG GCTCCTTGGG	1440
GCGGCGATGG TAGGGGCCGT CCTCACTGCC CTGCTGGCAG GGCTTGTGAG CTTGCTGTGT	1500
CGTCACAAGA GAAAGCAGCT TCCTGAAGAA AAGCAGCCAC TCCTCATGGA GAAAGAGGAT	1560
TACCACAGCT TGTATCAGAG CCATTTA	1587

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1587 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ATGCTCCTGG CTGTTTTGTA CTGCCTGCTG TGGAGTTTCC AGACCTCCGC TGGCCATTTTC	60
CCTAGAGCCT GTGTCTCCTC TAAGAACCTG ATGGAGAAGG AATGCTGTCC ACCGTGGAGC	120
GGGGACAGGA GTCCCTGTGG CCAGCTTTCA GGCAGAGGTT CCTGTCAGAA TATCCTTCTG	180
TCCAATGCAC CACTTGGGCC TCAATTTCCC TTCACAGGGG TGGATGACCG GGAGTCGTGG	240
CCTTCCGTCT TTTATAATAG GACCTGCCAG TGCTCTGGCA ACTTCATGGG ATTCAACTGT	300
GGAAACTGCA AGTTTGGCTT TTGGGGACCA AACTGCACAG AGAGACGACT CTTGGTGAGA	360
AGAAACATCT TCGATTTGAG TGCCCCAGAG AAGGACAAAT TTTTTCCTA CCTCACTTTA	420
GCAAAGCATA CCATCAGCTC AGACTATGTC ATCCCCATAG GGACCTATGG CCAAATGAAA	480
AATGGATCAA CACCCATGTT TAACGACATC AATATTTATG ACCTCTTTGT CTGGATGCAT	540
TATTATGTGT CAATGGATGC ACTGCTTGGG GGATATGAAA TCTGGAGAGA CATTGATTTT	600
GGCCATGAAG CACCAGCTTT TCTGCCCTGG CATAGACTCT TCTTGTTGCG GTGGGAACAA	660
GAAATCCAGA AGCTGACAGG AGATGAAAAC TTCACTATTC CATATTGGGA CTGGCGGGAT	720
GCAGAAAAGT GTGACATTTG CACAGATGAG TACATGGGAG GTCAGCACCC CACAAATCCT	780
AACTTACTCA GCCCAGCATC ATTCTTCTCC TCTTGGCAGA TTGTCTGTAG CCGATTGGAG	840
GAGTACAACA GCCATCAGTC TTTATGCAAT GGAACGCCCC AGGGACCTTT ACGGCGTAAT	900
CCTGGAAACC ATGACAAATC CAGAACCCCA AGGCTCCCCCT CTCAGCTGA TGTAGAATTT	960
TGCCTGAGTT TGACCCAATA TGAATCTGGT TCCATGGATA AAGCTGCCAA TTTCAGCTTT	1020
AGAAATACAC TGGAAGGATT TGCTAGTCCA CTTACTGGGA TAGCGGATGC CTCTCAAAGC	1080

AGCATGCACA ATGCCTTGCA CATCTATATG AATGGAACAA TGTCCCAGGT ACAGGGATCT 1140
 GCCAACGATC CTATCTTCCT TCTTCACCAT GCATTTGTTG ACAGTATTTT TGAGCAGTGG 1200
 CTCCGAAGGC ACCGTCCTCT TCAAGAAGTT TATCCAGAAG CCAATGCACC CATTGGACAT 1260
 AACCAGGAAT CCTACATGGT TCCTTTTATA CCACTGTACA GAAATGGTGA TTTCTTTATT 1320
 TCATCCAAAG ATCTGGGCTA TGA CTATAGC TATCTACAAG ATTCAGACCC AGACTCTTTT 1380
 CAAGACTACA TTAAGTCCTA TTTGGAACAA GCGAGTCGGA TCTGGTCATG GCTCCTTGGG 1440
 GCGGCGATGG TAGGGGCCGT CCTCACTGCC CTGCTGGCAG GGCTTGTGAG CTTGCTGTGT 1500
 CGTCACAAGA GAAAGCAGCT TCCTGAAGAA AAGCAGCCAC TCCTCATGGA GAAAGAGGAT 1560
 TACCACAGCT TGTATCAGAG CCATTTA 1587

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TAAATGGCTC TGATAAAGC T 21

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GCAAGTTTGG CTTTTGGGGA 20

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ATGCTCCTGG CTGTTTTGTA CTG 23

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CTGAATCTTG TAGATAGCTA TAGTCATAGC CCAGATCTTT GGATGAAATA AAGAAATCAC	60
CATTTCTGTA CAGTGGTATA AAAGGAACCA TGTAGGATTC CCGGTTATGT CTAATGGGTG	120
CATTGGCTTC TGGATAAACT TCTTGAAGAG GACGGTG	157

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CTGAATCTTG TAGATAGCTA TAGTCATAGC CCAGATCTTT GGATGAAATA AAGAAATCAC	60
CATTTCTGTA CAGTGGTATA AAAGGAACCA TGTAGGATTC CTGGTTATGT CCAATGGGTG	120
CATTGGCTTC TGGATAAACT TCTTGAAGAG GACGGTG	157

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GGTTGGCCAA TCTACTCCCA GG	22
--------------------------	----

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GCTCACTCAG TGTGGCAAAG	20
-----------------------	----

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GGTTGGCCAA TCTACTCCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC 60
AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT 120
CAAACAGACA CCATGGTGCA CCTGACTCCT GAGGAGAAGT CTGCCGTTAC TGCCCTGTGG 180
GGCAAGGTGA ACGTGGATGA AGTTGGTGGT GAGGCCCTGG GCAGGTGGT ATCAAGGTTA 240
CAAGACAGGT TTAAGGAGAC CAATAGAAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG 300
GTTTCTGATA GGCCTGACT CTCTCTGCCT ATTGGTCTAT TTTCCCACCC TTAGGCTGCT 360
GGTGGTCTAC CCTTGGACCC AGAGGTTCTT TGAGTCCTTT GGGGATCTGT CCACTCCTGA 420
TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCTTTAG 480
TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC 536

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GGTTGGCCAA TCTACTCCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC 60
AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT 120
CAAACAGACA CCATGGTGCA TCTGACTCCT GAGGAGGTCT GCCGTTACTG CCCTGTGGGG 180
CAAGGTGAAC GTGGATGAAG TTGGTGGTGA GGCCCTGGGC AGGTTGGTAT CAAGGTTACA 240
AGACAGGTTT AAGGAGACCA ATAGAACTG GGCATGTGGA GACAGAGAAG ACTCTTGGGT 300
TTCTGATAGG CACTGACTCT CTCTGCCTAT TGGTCTATTT TCCCACCCTT AGGCTGCTGG 360
TGGTCTACCC TTGGACCCAG AGGTTCTTTG AGTCCTTTGG GGATCTGTCC ACTCCTGATG 420
CTGTTATGGG CAACCCTAAG GTGAAGGCTC ATGGCAAGAA AGTGCTCGGT GCCTTTAGTG 480
ATGGCCTGGC TCACCTGGAC AACCTCAAGG GCACCTTTGC CACACTGAGT GAGC 534

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 536 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GGTTGGCCAA TCTACTCCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC	60
AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT	120
CAAACAGACA CCATGGTGCA CCTGACTCCT GAGGAGAAGT CTGCCGTTAC TGCCCTGTGG	180
GGCAAGGTGA ACGTGGATGA AGTTGGTGGT GAGGCCCTGG GCAGGTTGGT ATCAAGGTTA	240
CAAGACAGGT TTAAGGAGAC CAATAGAAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG	300
GTTTCTGATA GGCCTGACT CTCTCTGCCT ATTGGTCTAT TTTCCCACCC TTAGGCTGCT	360
GGTGGTCTAC CCTTGGACCT AGAGGTTCTT TGAGTCCTTT GGGGATCTGT CCACTCCTGA	420
TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCTTTAG	480
TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC	536

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 536 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GGTTGGCCAA TCTACTCCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC	60
AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT	120
CAAACAGACA CCATGGTGCA CCTGACTCCT GAGGAGAAGT CTGCCGTTAC TGCCCTGTGG	180
GGCAAGGTGA ACGTGGATGA AGTTGGAGGT GAGGCCCTGG GCAGGTTGGT ATCAAGGTTA	240
CAAGACAGGT TTAAGGAGAC CAATAGAAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG	300
GTTTCTGATA GGCCTGACT CTCTCTGCCT ATTGGTCTAT TTTCCCACCC TTAGGCTGCT	360
GGTGGTCTAC CCTTGGACCC AGAGGTTCTT TGAGTCCTTT GGGGATCTGT CCACTCCTGA	420
TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCTTTAG	480
TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC	536

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GAAUACUCAA GCUUGCAUGC CUGCAGGUCG ACUCUAGAGG AUCCCCGGGU ACCGAGCUCG 60

AAUU 64

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GGCTGACAAG AAGGAACTC 20

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CCAGGCGGCG GCTAGGAGAG ATGGG 25

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GGCTGACAAG AAGGAACTC GCTGAGACAG CAGGGACTTT CCACAAGGGG ATGTTACGGG 60

GAGGTACTGG GGAGGAGCCG GTCGGGAACG CCCACTCTCT TGATGTATAA ATATCACTGC 120

ATTTCGCTCT GTATTAGTC GCTCTGCGGA GAGGCTGGCA GATTGAGCCC TGGGAGGTTC 180

TCTCCAGCAC TAGCAGGTAG AGCCTGGGTG TTCCCTGCTA GACTCTCACC AGCACTTGGC 240

CGGTGCTGGG CAGAGTGGCT CCACGCTTGC TTGCTTAAAG ACCTCTTCAA TAAAGCTGCC 300

ATTTTAGAAG TAGGCCAGTG TGTGTTCCCA TCTCTCCTAG CCGCCGCCTG G

351

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GGCTGACAAG AAGGAAACTC GCTGAGATAG CAGGGACTTT CCACAAGGGG ATGTTATGGG	60
GAGGAGCCGG TCGGGAACAC CCACTTTCTT GATGTATAAA TATCACTGCA TTTCGCTCTG	120
TATTCAGTCG CTCTGCGGAG AGGCTGGCAG ATTGAGCCCT GGGAGGTTCT CTCCAGCACT	180
AGCAGGTAGA GCCTGGGTGT TCCCTGCTAG ACTCTCACCA GCACTTAGCC AGTGCTGGGC	240
AGAGTGGCTC CACGCTTGCT TGCTTAAAGA CCTCTTCAAT AAAGCTGCCA TTTTAGAAGT	300
AAGCCAGTGT GTGTTCCCAT CTCTCCTAGC CGCCGCCTGG	340

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GGCTGACAAG AAGGAAACTC GCTGAGATAG CAGGGACTTT CCACAAGGGG ATGTTATGGG	60
GAGGAGCCGG TCGGGAACAC CCACTTTCTT GGTGTATAAA TATCACTGCA TTTCGCTCTG	120
TATTCAGTCG CTCTGCGGAG AGGCTGGCAG ATTGAGCCCT GGGAGGTTCT CTCCAGCACT	180
AGCAGGTAGA GCCTGGGTGT TCCCTGCTAG ACTCTCACCA GCACTTGGCC AGTGCTGGGC	240
AGAGTGGCTC CACGCTTGCT TGCTTAAAGA CCTCTTCAAT AAAGCTGCCA TTTTAGAAGT	300
AAGCCAGTGT GTGTTCCCAT CTCTCCTAGC CGCCGCCTGG	340

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GGCTGACAAG AAGGAACTC GCTGAGACAG CAGGGACTTT CCACAAGGGG ATGTTACGGG 60
 GAGGTACTGG GGAGGAGCCG GTCGGGAACG CCCCTCTCT TGATGTATAA ATATCACTGC 120
 ATTTGCTCT GTATTCAGTC GCTCTGCGGA GAGGCTGGCA GATTGAGCCC TGGGAGGTTC 180
 TCTCCAGCAC TAGCAGGTAG AGCCTGGGTG TTCCCTGCTA GACTCTCACC AGCACTTGGC 240
 CGGTGCTGGG CAGAGTGGCT CCACGCTTGC TTGCTTAAAG ACCTCTTCAA TAAAGCTGCC 300
 ATTTTAGAAG TAGGCTAGTG TGTGTTCCCA TCTCTCCTAG CCGCCGCCTG G 351

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GGCTGACAAG AAGGAACTC GCTGAAACAG CAGGGACTTT CCACAAGGGG ATGTTACGGG 60
 GAGGTACTGG GAAGGAGCCG GTCGGGAACG CCCACTTTCT TGATGTATAA ATATCACTGC 120
 ATTTGCTCT GTATTCAGTC GCTCTGCGGA GAGGCTGGCA GATTGAGCCC TGGGAGGTTC 180
 TCTCCAGCAC TAGCAGGTAG AGCCTGGGTG TTCCCTGCTA GACTCTCACC AGCACTTGGC 240
 CGGTGCTGGG CAGAGTGA CT CCACGCTTGC TTGCTTAAAG CCCTCTTCAA TAAAGCTGCC 300
 ATTTTAGAAG TAAGCTAGTG TGTGTTCCCA TCTCTCCTAG CCGCCGCCTG G 351

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GGCTGACAAG AAGGAACTC GCTGAGACAG CAGGGACTTT CCACAAGGGG ATGTTACGGA 60
 GAGGTACTGG GGAGGAGCCG GTCGGGAACG CCCACTCTCT TGATGTATAA ATATCACTGC 120
 ATTTGCTCT GTATTCAGTC GCTCTGCGGA GAGGCTGGCA GATTGAGCCC TAGGAGGTTC 180
 TCTCCAGCAC TAGCAGGTAG AGCCTGAGTG TTCCCTGCTA AACTCTCACC AGCACTTGGC 240
 CGGTGCTGGG CAGAGCGGCT CCACGCTTGC TTGCTTAAAG ACCTCTTCAA TAAAGCTGCC 300
 ATTTTAGAAG TAGGCTAGTG TGTGTTCCCA TCTCTCCTAG CCGCCGCCTG G 351

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 536 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

```
GGTTGGCCAA TCTACTCCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC      60
AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT      120
CAAACAGACA CCATGGTGCA TCTGACTCCT GAGGAGAAGT CTGCCGTTAC TGCCCTGTGG      180
GGCAAGGTGA ACGTGGATGA AGTTGGTGGT AAGGCCCTGG GCAGGTTGGT ATCAAGGTTA      240
CAAGACAGGT TTAAGGAGAC CAATAGAAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG      300
GTTTCTGATA GGCCTGACT CTCTCTGCCT ATTGGTCTAT TTTCCCACCC TTAGGCTGCT      360
GGTGGTCTAC CCTTGGACCC AGAGGTTCTT TGAGTCCTTT GGGGATCTGT CCACTCCTGA      420
TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCTTTAG      480
TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC      536
```

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 536 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```
GGTTGGCCAA TCTACTCCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC      60
AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT      120
CAAACAGACA CCATGGTGCA CCTGACTCCT GAGGAGAAGT CTGCCGTTAC TGCCCTGTGG      180
GGCAAGGTGA ACGTGGATGA AGTTGGTGGT GAGGCCCTGG GCAGGTTGGT ATCAAGGTTA      240
CAAGACAGGT TTAAGGAGAC CAATAGAAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG      300
GTTTCTGATA GGCCTGACT CTCTCTGCCT ATTAGTCTAT TTTCCCACCC TTAGGCTGCT      360
GGTGGTCTAC CCTTGGACCC AGAGGTTCTT TGAGTCCTTT GGGGATCTGT CCACTCCTGA      420
TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCTTTAG      480
TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC      536
```

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 157 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCAGGAA	60
TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA	120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAG	157

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 833 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu	1	5	10	15
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys	20	25	30	
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe	35	40	45	
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile	50	55	60	
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly	65	70	75	80
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln	85	90	95	
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu	100	105	110	
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys	115	120	125	
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys	130	135	140	
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu	145	150	155	160
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg	165	170	175	
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp	180	185	190	

Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
 530 535 540
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Arg Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Glu

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 548 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	1	5	10	15
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	20	25	30	
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	35	40	45	
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	50	55	60	
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	65	70	75	80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	85	90	95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu	100	105	110	
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	115	120	125	
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	130	135	140	
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	145	150	155	160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	165	170	175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	180	185	190	
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	195	200	205	
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	210	215	220	
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	225	230	235	240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	245	250	255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala	260	265	270	
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	275	280	285	

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
 355 360 365
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
 405 410 415
 Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
 420 425 430
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
 450 455 460
 Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln Ala Cys Lys Leu Gly Thr Gly Arg Arg
 530 535 540
 Phe Thr Thr Ser
 545

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 695 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65					70					75					80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
145					150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
				165					170					175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp
			180					185					190		
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu
		195					200					205			
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg
	210					215					220				
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu
225					230					235					240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu
				245					250					255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala
			260					265					270		
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu
		275					280					285			
Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu
	290					295					300				
Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala
305					310					315					320
Asp	Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala
				325					330					335	

Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
340 345 350

Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
355 360 365

Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
385 390 395 400

Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
405 410 415

Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
420 425 430

Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
435 440 445

Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
450 455 460

Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
485 490 495

Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
515 520 525

Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
530 535 540

Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
580 585 590

Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
625 630 635 640

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ser His Pro Leu
675 680 685

Arg Gly Gly Pro Gly Leu His
690 695

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
100 105 110
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
115 120 125
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
180 185 190
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
195 200 205
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
210 215 220
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
225 230 235 240

Parameter	Value	Unit
Temperature	25.0	°C
Pressure	1.0	atm
Flow rate	1.0	L/min
Concentration	0.1	mol/L
pH	7.0	
Wavelength	254	nm
Scan rate	10	nm/min
Integration time	10	s
Resolution	0.5	nm
Slit width	1.0	nm
Detector	Photodiode array	
Software	Chromatography	
Hardware	PC/AT	
Operating system	Windows 95	
Database	Chemical	
Search method	Library	
Identification	Yes	
Confidence	95	%
Limit of detection	0.1	µg/L
Limit of quantitation	0.5	µg/L
Recovery	100	%
Stability	1.0	min
Reproducibility	1.0	%
Linearity	1.0	%
Specificity	1.0	%
Sensitivity	1.0	%
Robustness	1.0	%
Reliability	1.0	%
Accuracy	1.0	%
Precision	1.0	%
Resolution	1.0	%
Stability	1.0	%
Reproducibility	1.0	%
Linearity	1.0	%
Specificity	1.0	%
Sensitivity	1.0	%
Robustness	1.0	%
Reliability	1.0	%
Accuracy	1.0	%
Precision	1.0	%
Resolution	1.0	%
Stability	1.0	%
Reproducibility	1.0	%
Linearity	1.0	%
Specificity	1.0	%
Sensitivity	1.0	%
Robustness	1.0	%
Reliability	1.0	%
Accuracy	1.0	%
Precision	1.0	%
Resolution	1.0	%
Stability	1.0	%
Reproducibility	1.0	%
Linearity	1.0	%
Specificity	1.0	%
Sensitivity	1.0	%
Robustness	1.0	%
Reliability	1.0	%
Accuracy	1.0	%
Precision	1.0	%
Resolution	1.0	%
Stability	1.0	%
Reproducibility	1.0	%
Linearity	1.0	%
Specificity	1.0	%
Sensitivity	1.0	%
Robustness	1.0	%
Reliability	1.0	%
Accuracy	1.0	%
Precision	1.0	%
Resolution	1.0	%
Stability	1.0	%
Reproducibility	1.0	%
Linearity	1.0	%
Specificity	1.0	%
Sensitivity	1.0	%
Robustness	1.0	%
Reliability	1.0	%
Accuracy	1.0	%
Precision	1.0	%
Resolution	1.0	%
Stability	1.0	%
Reproducibility	1.0	%
Linearity	1.0	%
Specificity	1.0	%
Sensitivity	1.0	%
Robustness	1.0	%
Reliability	1.0	%
Accuracy	1.0	%
Precision	1.0	%
Resolution	1.0	%
Stability	1.0	%
Reproducibility	1.0	%
Linearity	1.0	%
Specificity	1.0	%
Sensitivity	1.0	%
Robustness	1.0	%
Reliability	1.0	%
Accuracy	1.0	%
Precision	1.0	%
Resolution	1.0	%
Stability	1.0	%
Reproducibility	1.0	%
Linearity	1.0	%
Specificity	1.0	%
Sensitivity	1.0	%
Robustness	1.0	%
Reliability	1.0	%
Accuracy	1.0	%
Precision	1.0	%
Resolution	1.0	%
Stability	1.0	%
Reproducibility	1.0	%
Linearity	1.0	%
Specificity	1.0	%
Sensitivity	1.0	%
Robustness	1.0	%
Reliability	1.0	%
Accuracy	1.0	%
Precision	1.0	%
Resolution	1.0	%
Stability	1.0	%
Reproducibility	1.0	%
Linearity	1.0	%
Specificity	1.0	%
Sensitivity	1.0	%
Robustness	1.0	%
Reliability	1.0	%
Accuracy	1.0	%
Precision	1.0	%
Resolution	1.0	%
Stability	1.0	%
Reproducibility	1.0	%
Linearity	1.0	%
Specificity	1.0	%
Sensitivity	1.0	%

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

- 361 -

Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu Pro Gly
195 200 205

Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp
210 215 220

Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala
225 230 235 240

Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu Ser Trp
245 250 255

Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp Phe Ala
260 265 270

Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe Leu Glu Arg
275 280 285

Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro
290 295 300

Lys Ser Trp Arg Gly Cys Ile Pro Trp Pro Cys Pro Trp Arg Trp Arg
305 310 315 320

Trp Gly

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 528 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly
1 5 10 15

His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr
20 25 30

Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu
35 40 45

Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp
50 55 60

Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr Lys Ala
65 70 75 80

Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala Leu Ile
85 90 95

Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu Val Pro Gly
100 105 110

Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys Ala Glu Lys
115 120 125

Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu Tyr Gln
 130 135 140
 Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr Leu Ile
 145 150 155 160
 Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp Gln Trp
 165 170 175
 Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu Pro Gly
 180 185 190
 Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp
 195 200 205
 Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala
 210 215 220
 Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu Ser Trp
 225 230 235 240
 Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp Phe Ala
 245 250 255
 Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe Leu Glu Arg
 260 265 270
 Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro
 275 280 285
 Lys Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala
 290 295 300
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
 305 310 315 320
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr
 325 330 335
 Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro
 340 345 350
 Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
 355 360 365
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
 370 375 380
 Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
 385 390 395 400
 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val
 405 410 415
 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg
 420 425 430
 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
 435 440 445
 Val Arg Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
 450 455 460

Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His
465 470 475 480

Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala
485 490 495

Arg Leu Ala Lys Glu Val Met Gly Gly Val Tyr Pro Leu Ala Val Pro
500 505 510

Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu
515 520 525

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser Gly
1 5 10 15

Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly
20 25 30

His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr
35 40 45

Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu
50 55 60

Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp
65 70 75 80

Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr Lys Ala
85 90 95

Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala Leu Ile
100 105 110

Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu Val Pro Gly
115 120 125

Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys Ala Glu Lys
130 135 140

Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu Tyr Gln
145 150 155 160

Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr Leu Ile
165 170 175

Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp Gln Trp
180 185 190

Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu Pro Gly
195 200 205

Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp
 210 215 220

Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala
 225 230 235 240

Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu Ser Trp
 245 250 255

Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp Phe Ala
 260 265 270

Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe Leu Glu Arg
 275 280 285

Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro
 290 295 300

Lys Ala Ala Leu Glu His His His His His
 305 310 315

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1182 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATGGAGGAGC CGCAGTCAGA TCCTAGCGTC GAGCCCCCTC TGAGTCAGGA AACATTTTCA	60
GACCTATGGA AACTACTTCC TGAAAACAAC GTTCTGTCCC CCTTGCCGTC CCAAGCAATG	120
GATGATTTGA TGCTGTCCCC GGACGATATT GAACAATGGT TCACTGAAGA CCCAGGTCCA	180
GATGAAGCTC CCAGAATGCC AGAGGCTGCT CCCCCGTGG CCCCTGCACC AGCAGCTCCT	240
ACACCGGCGG CCCCTGCACC AGCCCCCTCC TGGCCCCCTGT CATCTTCTGT CCCTTCCCAG	300
AAAACCTACC AGGGCAGCTA CGGTTTCCGT CTGGGCTTCT TGCATTCTGG GACAGCCAAG	360
TCTGTGACTT GCACGTACTC CCCTGCCCTC AACAAGATGT TTTGCCAACT GGCCAAGACC	420
TGCCCTGTGC AGCTGTGGGT TGATTCCACA CCCCCGCCCC GCACCCGCGT CCGCGCCATG	480
GCCATCTACA AGCAGTCACA GCACATGACG GAGGTTGTGA GGCCTGCCCC CCACCATGAG	540
CGCTGCTCAG ATAGCGATGG TCTGGCCCCCT CCTCAGCATC TTATCCGAGT GGAAGGAAAT	600
TTGCGTGTGG AGTATTTGGA TGACAGAAAC ACTTTTCGAC ATAGTGTGGT GGTGCCCTAT	660
GAGCCGCCTG AGGTTGGCTC TGA CTGTACC ACCATCCACT ACAACTACAT GTGTAACAGT	720
TCCTGCATGG GCGGCATGAA CCGGAGGCCC ATCCTCACCA TCATCACACT GGAAGACTCC	780
AGTGGTAATC TACTGGGACG GAACAGCTTT GAGGTGCGTG TTTGTGCCTG TCCTGGGAGA	840
GACCGGCGCA CAGAGGAAGA GAATCTCCGC AAGAAAGGGG AGCCTCACCA CGAGCTGCCC	900

CCAGGGAGCA CTAAGCGAGC ACTGCCCAAC AACACCAGCT CCTCTCCCCA GCCAAAGAAG 960
 AAACCACTGG ATGGAGAATA TTTCACCCTT CAGATCCGTG GCGGTGAGCG CTTCGAGATG 1020
 TTCCGAGAGC TGAATGAGGC CTTGGAATC AAGGATGCCC AGGCTGGGAA GGAGCCAGGG 1080
 GGGAGCAGGG CTCACTCCAG CCACCTGAAG TCCAAAAAGG GTCAGTCTAC CTCCCGCCAT 1140
 AAAAACTCA TGTTCAAGAC AGAAGGGCCT GACTCAGACT GA 1182

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1182 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATGGAGGAGC CGCAGTCAGA TCCTAGCGTC GAGCCCCCTC TGAGTCAGGA AACATTTTCA 60
 GACCTATGGA AACTACTTCC TGAAAACAAC GTTCTGTCCC CCTTGCCGTC CCAAGCAATG 120
 GATGATTTGA TGCTGTCCCC GGACGATATT GAACAATGGT TCACTGAAGA CCCAGGTCCA 180
 GATGAAGCTC CCAGAATGCC AGAGGCTGCT CCCCCGTGG CCCCTGCACC AGCAGCTCCT 240
 ACACCGGCGG CCCCTGCACC AGCCCCCTCC TGGCCCCCTGT CATCTTCTGT CCCTTCCCAG 300
 AAAACCTACC AGGGCAGCTA CGGTTTCCGT CTGGGCTTCT TGCATTCTGG GACAGCCAAG 360
 TCTGTGACTT GCACGTACTC CCCTGCCCTC AACAAGATGT TTTGCCAACT GGCCAAGACC 420
 TGCCCTGCGC AGCTGTGGGT TGATTCCACA CCCCCGCCC GCACCCGCGT CCGCGCCATG 480
 GCCATCTACA AGCAGTCACA GCACATGACG GAGGTTGTGA GCGCTGCCC CCACCATGAG 540
 CGTGCTCAG ATAGCGATGG TCTGGCCCCCT CCTCAGCATC TTATCCGAGT GGAAGGAAAT 600
 TTGCGTGTGG AGTATTTGGA TGACAGAAAC ACTTTTCGAC ATAGTGTGGT GGTGCCCTAT 660
 GAGCCGCCTG AGGTTGGCTC TGAATGTACC ACCATCCACT ACAACTACAT GTGTAACAGT 720
 TCCTGCATGG GCGGCATGAA CCGGAGGCCC ATCCTCACCA TCATCACACT GGAAGACTCC 780
 AGTGGTAATC TACTGGGACG GAACAGCTTT GAGGTGCGTG TTTGTGCCTG TCCTGGGAGA 840
 GACCGGCGCA CAGAGGAAGA GAATCTCCGC AAGAAAGGGG AGCCTCACCA CGAGCTGCCC 900
 CCAGGGAGCA CTAAGCGAGC ACTGCCCAAC AACACCAGCT CCTCTCCCCA GCCAAAGAAG 960
 AAACCACTGG ATGGAGAATA TTTCACCCTT CAGATCCGTG GCGGTGAGCG CTTCGAGATG 1020
 TTCCGAGAGC TGAATGAGGC CTTGGAATC AAGGATGCCC AGGCTGGGAA GGAGCCAGGG 1080
 GGGAGCAGGG CTCACTCCAG CCACCTGAAG TCCAAAAAGG GTCAGTCTAC CTCCCGCCAT 1140
 AAAAACTCA TGTTCAAGAC AGAAGGGCCT GACTCAGACT GA 1182

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATGGAGGAGC CGCAGTCAGA TCCTAGCGTC GAGCCCCCTC TGAGTCAGGA AACATTTTCA 60
GACCTATGGA AACTACTTCC TGAAAACAAC GTTCTGTCCC CTTTGCCGTC CCAAGCAATG 120
GATGATTTGA TGCTGTCCCC GGACGATATT GAACAATGGT TCACTGAAGA CCCAGGTCCA 180
GATGAAGCTC CCAGAATGCC AGAGGCTGCT CCCCCGTGG CCCCTGCACC AGCAGCTCCT 240
ACACCGGCGG CCCCTGCACC AGCCCCCTCC TGGCCCCGTG CATCTTCTGT CCCTTCCCAG 300
AAAACCTACC AGGGCAGCTA CGGTTTCCGT CTGGGCTTCT TGCATTCTGG GACAGCCAAG 360
TCTGTGACTT GCACGTACTC CCCTGCCCTC AACAAGATGT TTTGCCAACT GGCCAAGACC 420
TGCCCTGTGC AGCTGTGGGT TGATTCCACA CCCCCGCCG GCACCCGCGT CCGCGCCATG 480
GCCATCTACA AGCAGTCACA GCACATGACG GAGGTGTGTA GGCCTGCCCC CCACCATGAG 540
CGCTGCTCAG ATAGCGATGG TCTGGCCCCCT CCTCAGCATC TTATCCGAGT GGAAGGAAAT 600
TTGCGTGTGG AGTATTTGGA TGACAGAAAC ACTTTTCGAC ATAGTGTGGT GGTGCCCTAT 660
GAGCCGCCTG AGGTTGGCTC TGACTGTACC ACCATCCACT ACAACTACAT GTGTAACAGT 720
TCCTGCATGG GCGGCATGAA CCGGAGACCC ATCCTCACCA TCATCACACT GGAAGACTCC 780
AGTGGTAATC TACTGGGACG GAACAGCTTT GAGGTGCGTG TTTGTGCCTG TCCTGGGAGA 840
GACCGGCGCA CAGAGGAAGA GAATCTCCGC AAGAAAGGGG AGCCTCACCA CGAGCTGCCC 900
CCAGGGAGCA CTAAGCGAGC ACTGCCCAAC AACACCAGCT CCTCTCCCCA GCCAAAGAAG 960
AAACCACTGG ATGGAGAATA TTTCACCCTT CAGATCCGTG GGCGTGAGCG CTTCGAGATG 1020
TTCCGAGAGC TGAATGAGGC CTTGGAATC AAGGATGCCC AGGCTGGGAA GGAGCCAGGG 1080
GGGAGCAGGG CTCACTCCAG CCACCTGAAG TCCAAAAAGG GTCAGTCTAC CTCCCGCCAT 1140
AAAAAACTCA TGTTCAGAC AGAAGGGCCT GACTCAGACT GA 1182

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TCTGGGCTTC TTGCATTCTG

20

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GTTGGGCAGT GCTCGCTTAG

20

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT	60
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC	120
ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC	180
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC	240
TCCTCAGCAT CTTATCCGAG TGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA	300
CACTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC	360
CACCATCCAC TACAACTACA TGTGTAACAG TTCTGCATG GGCGGCATGA ACCGGAGGCC	420
CATCCTCACC ATCATCACAC TGAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT	480
TGAGGTGCGT GTTTGTGCCT GTCCTGGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG	540
CAAGAAAGGG GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCCAA	600
C	601

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTTCTT	60
GCGGAGATTC TCTTCCTCTG TGCGCCGGTC TCTCCAGGA CAGGCACAAA CACGCACCTC	120
AAAGCTGTTC CGTCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT	180
GGGCCTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT	240
GGTACAGTCA GAGCCAACCT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT	300
GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCTTCC ACTCGGATAA GATGCTGAGG	360
AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGGCAGCGCC TCACAACCTC	420
CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGGG	480
TGTGGAATCA ACCCAGAGCT GCACAGGGCA GGTCTTGGCC AGTTGGCAA ACATCTTGTT	540
GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCCAG	600
A	601

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT	60
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGCG CAGCTGTGGG TTGATTCCAC	120
ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC	180
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC	240
TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA	300
CACTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC	360
CACCATCCAC TACAATACTA TGTGTAACAG TTCCTGCATG GGCGGCATGA ACCGGAGGCC	420
CATCCTCACC ATCATCACAC TGGAAGACTC CAGTGTAAT CTACTGGGAC GGAACAGCTT	480
TGAGGTGCGT GTTTGTGCCT GTCCTGGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG	540
CAAGAAAGGG GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCCAA	600
C	601

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTTCTT	60
GCGGAGATTC TCTTCCTCTG TGCGCCGGTC TCTCCCAGGA CAGGCACAAA CACGCACCTC	120
AAAGCTGTTC CGTCCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT	180
GGGCTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT	240
GGTACAGTCA GAGCCAACCT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT	300
GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCTTCC ACTCGGATAA GATGCTGAGG	360
AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGGCAGCGCC TCACAACCTC	420
CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGGG	480
TGTGGAATCA ACCCACAGCT GCGCAGGGCA GGTCTTGGCC AGTTGGCAA ACATCTTGTT	540
GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCCAG	600
A	601

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 601 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT	60
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC	120
ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC	180
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC	240
TCCTCAGCAT CTTATCCGAG TGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA	300
CACTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC	360
CACCATCCAC TACAACCTACA TGTGTAACAG TTCCTGCATG GGCGGCATGA ACCGGAGACC	420
CATCCTCACC ATCATCACAC TGGAAGACTC CAGTGGTAAT CTAAGGGAC GGAACAGCTT	480
TGAGGTGCGT GTTTGTGCCT GTCCTGGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG	540
CAAGAAAGGG GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCCAA	600

C

601

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 601 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GTGGGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTTCTT	60
GCGGAGATTG TCTTCCTCTG TGCGCCGGTC TCTCCCAGGA CAGGCACAAA CACGCACCTC	120
AAAGCTGTTC CGTCCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT	180
GGGTCTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT	240
GGTACAGTCA GAGCCAACCT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT	300
GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCTTCC ACTCGGATAA GATGCTGAGG	360
AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGCAGCGCC TCACAACCTC	420
CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGGG	480
TGTGGAATCA ACCCAGCT GCACAGGGCA GGTCTTGGCC AGTTGGCAAA ACATCTTGTT	540
GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCAG	600
A	601

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GAGGATGGGA CTCCGGTTCA TG	22
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(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

C

601

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

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GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGCAGCTCG TGGTGAGGCT CCCCTTTCTT      60
GCGGAGATTC TCTTCCTCTG TCGCCCGGTC TCTCCAGGA CAGGCACAAA CACGCACCTC      120
AAAGCTGTTT CGTCCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT      180
GGGACTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT      240
GGTACAGTCA GAGCCAACCT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT      300
GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCTTCC ACTCGGATAA GATGCTGAGG      360
AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGCAGCGCC TCACAACCTC      420
CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGGG      480
TGTGGAATCA ACCCAGCT GCACAGGGCA GGTCTTGGCC AGTTGGCAA ACATCTTGT      540
GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCCAG      600
A                                                                                   601

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(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

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TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT      60
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC      120
ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC      180
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC      240
TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA      300
CACTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC      360
CACCATCCAC TACAACCTACA TGTGTAACAG TTCCTGCATG GCGGCATGA ACCGGAGGCC      420

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CATCCTCACC ATCATCACAC TGGAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT 480
 TGAGGTGCAT GTTTGTGCCT GTCCTGGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG 540
 CAAGAAAGGG GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCCAA 600
 C 601

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTTCTT 60
 GCGGAGATTC TCTTCCTCTG TGCGCCGGTC TCTCCAGGA CAGGCACAAA CATGCACCTC 120
 AAAGCTGTTT CGTCCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT 180
 GGGCCTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT 240
 GGTACAGTCA GAGCCAACCT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT 300
 GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCCCTTCC ACTCGGATAA GATGCTGAGG 360
 AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGGCAGCGCC TCACAACCTC 420
 CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGGG 480
 TGTGGAATCA ACCCACAGCT GCACAGGGCA GGTCTTGGCC AGTTGGCAAA ACATCTTGTT 540
 GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCCAG 600
 A 601

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 427 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT 60
 CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC 120
 ACCCCCGCCG GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC 180
 GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC 240

TCCTCAGCAT CTTATCCGAG TGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA 300
 CACTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC 360
 CACCATCCAC TACAACTACA TGTGTAACAG TTCCTGCATG GCGGCATGA ACCGGAGTCC 420
 CATCCTC 427

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 196 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CATGAACCGG AGTCCCATCC TCACCATCAT CACACTGGAA GACTCCAGTG GTAATCTACT 60
 GGGACGGAAC AGCTTTGAGG TCGTGTTTG TGCCTGTCCT GGGAGAGACC GCGGCACAGA 120
 GGAAGAGAAT CTCCGCAAGA AAGGGGAGCC TCACCACGAG CTGCCCCCAG GGAGCACTAA 180
 GCGAGCACTG CCCAAC 196

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 498 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT 60
 CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC 120
 ACCCCCCGCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC 180
 GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC 240
 TCCTCAGCAT CTTATCCGAG TGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA 300
 CACTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC 360
 CACCATCCAC TACAACTACA TGTGTAACAG TTCCTGCATG GCGGCATGA ACCGGAGGCC 420
 CATCCTCACC ATCATCACAC TGGAAGACTC CAGTGGTAACT CTACTGGGAC GGAACAGCTT 480
 TGAGGTGCAT GTTTGTGC 498

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 127 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

CAGCTTTGAG GTGCATGTTT GTGCCTGTCC TGGGAGAGAC CGGCGCACAG AGGAAGAGAA 60
TCTCCGCAAG AAAGGGGAGC CTCACCACGA GCTGCCCCCA GGGAGCACTA AGCGAGCACT 120
GCCCAAC 127

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GGTTTTTCTT TGAGGTTTAG 20

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GCGACACTCC ACCATAGAT 19

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

CTGTCTTCAC GCAGAAAGC 19

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

[illegible]

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

19

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

60

120

180

240

281

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 386 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

CTGTCTTCAC GCAGAAAGCG TCTGGCCATG GCGTTAGTAT GAGTGTCGTG CAGCCTCCAG	60
GACCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGACTGTC TTCACGCAGA	120
AAGCGTCTAG CCATGGCGTT AGTATGAGTG TCGTGACGCC TCCAGGACCC CCCCTCCCGG	180
GAGAGCCATA GTGGTCTGCG GAACCGGTGA GTACACCGGA ATTGCCAGGA CGACCGGGTC	240
CTTTCTTGGA TCAACCCGCT CAATGCCTGG AGATTTGGGC GTGCCCCCGC AAGACTGCTA	300
GCCGAGTAGT GTTGGGTGCG GAAAGGCCTT GTGGTACTGC CTGATAGGGT GCTTGCGAGT	360
GCCCCGGGAG GTCTCGTAGA CCGTGC	386

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 281 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCGTG CAGCCTCCAG	60
GTCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	120
CAGGACGACC GGGTCCTTTC TTGGATCAAC CCGCTCAATG CCTGGAGATT TGGGCGTGCC	180
CCCCGCGAGAC TGCTAGCCGA GTAGTGTGG GTGCGGAAAG GCCTTGTGGT ACTGCCTGAT	240
AGGGTGCTTG CGAGTGCCCC GGGAGGTCTC GTAGACCGTG C	281

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 282 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCGTG CAGCCTCCAG	60
GACCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	120
CAGGACGACC GGGTCCTTTC GTGGATGTAA CCCGCTCAAT GCCTGGAGAT TTGGGCGTGC	180

CCCCGCAAGA CTGCTAGCCG AGTAGTGTG GGTGCGGAAA GGCCTTGTGG TACTGCCTGA 240
TAGGGTGCTT GCGAGTGCCC CGGGAGGTCT CGTAGACCGT GC 282

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTGTA CAGCCTCCAG 60
GCCCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC 120
CGGGAAGACT GGGTCCTTTC TTGGATAAAC CCACTCTATG CCCGGCCATT TGGGCGTGCC 180
CCCGCAAGAC TGCTAGCCGA GTAGCGTTGG GTTGCGAAAG GCCTTGTGGT ACTGCCTGAT 240
AGGGTGCTTG CGAGTACCCC GGGAGGTCTC GTAGACCGTG C 281

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CTGTCTTCAC GCAGAAAGCG CCTAGCCATG GCGTTAGTAC GAGTGTGTA CAGCCTCCAG 60
GACCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC 120
TGGGGTGACC GGGTCCTTTC TTGGAGCAAC CCGCTCAATA CCCAGAAATT TGGGCGTGCC 180
CCCGCGAGAT CACTAGCCGA GTAGTGTGG GTGCGGAAAG GCCTTGTGGT ACTGCCTGAT 240
AGGGTGCTTG CGAGTGCCCC GGGAGGTCTC GTAGACCGTG C 281

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAGGCACCC TATCAGGCAG TACCACAAGG 60

CCTTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTTGCGG GGGCACGCCC AAATCTCCAG 120
 GCATTGAGCG GGTTTATCCA AGAAAGGACC CGGTCGTCCT GGCAATTCCG GTGTACTCAC 180
 CGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGGT CCTGGAGGCT GCACGACACT 240
 CATACTAACG CCATGGCCAG ACGCTTTCTG CGTGAAGACA G 281

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAAGCACCC TATCAGGCAG TACCACAAGG 60
 CCTTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTTGCGG GGGCACGCCC AAATCTCCAG 120
 GCATTGAGCG GGTTGATCCA AGAAAGGACC CGGTCGTCCT GGCAATTCCG GTGTACTCAC 180
 CGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGGT CCTGGAGGCT GCACGACACT 240
 CATACTAACG CCATGGCTAG ACGCTTTCTG CGTGAAGACA G 281

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAAGCACCC TATCAGGCAG TACCACAAGG 60
 CCTTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTGCGG GGGCACGCCC AAATCTCCAG 120
 GCATTGAGCG GGTTGATCCA AGAAAGGACC CGGTCGTCCT GGCAATTCCG GTGTACTCAC 180
 CGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGGA CCTGGAGGCT GCACGACACT 240
 CATACTAACG CCATGGCTAG ACGCTTTCTG CGTGAAGACA G 281

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAAGCACCC TATCAGGCAG TACCACAAGG	60
CCTTTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTTGCGG GGGCACGCCC AAATCTCCAG	120
GCATTGAGCG GGTACATCC ACGAAAGGAC CCGGTCGTCC TGGCAATTCC GGTGTACTCA	180
CCGGTTCCGC AGACCACTAT GGCTCTCCCG GGAGGGGGGG TCCTGGAGGC TGCACGACAC	240
TCATACTAAC GCCATGGCTA GACGCTTTCT GCGTGAAGAC AG	282

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GCACGGTCTA CGAGACCTCC CGGGGTACTC GCAAGCACCC TATCAGGCAG TACCACAAGG	60
CCTTTTCGCAA CCCAACGCTA CTCGGCTAGC AGTCTTGCGG GGGCACGCCC AAATGGCCGG	120
GCATAGAGTG GGTTTATCCA AGAAAGGACC CAGTCTTCCC GGCAATTCCG GTGTACTCAC	180
CGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGGG CCTGGAGGCT GTACGACACT	240
CATACTAACG CCATGGCTAG ACGCTTTCTG CGTGAAGACA G	281

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAAGCACCC TATCAGGCAG TACCACAAGG	60
CCTTTTCGCGA CCCAACACTA CTCGGCTAGT GATCTCGCGG GGGCACGCCC AAATTTCTGG	120
GTATTGAGCG GGTGCTCCA AGAAAGGACC CGGTCACCCC AGCGATTCCG GTGTACTCAC	180
CGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGGT CCTGGAGGCT GCACGACACT	240
CGTACTAACG CCATGGCTAG GCGCTTTCTG CGTGAAGACA G	281

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

ATCAACATCC GGCCGGTGGT

20

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GGGGCCTCGC TACGGACCAG

20

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 620 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ATCAACATCC GGCCGGTGGT CGCCGCGATC AAGGAGTTCT TCGGCACCAG CCAGCTGAGC	60
CAATTCATGG ACCAGAACAA CCCGCTGTCG GGGTTGACCC ACAAGCGCCG ACTGTCGGCG	120
CTGGGGCCCCG GCGGTCTGTC ACGTGAGCGT GCCGGGCTGG AGGTCCGCGA CGTGCACCCG	180
TCGCACTACG GCCGGATGTG CCCGATCGAA ACCCCTGAGG GGCCCAACAT CGGTCTGATC	240
GGCTCGCTGT CGGTGTACGC GCGGGTCAAC CCGTTCGGGT TCATCGAAAC GCCGTACCGC	300
AAGGTGGTCG ACGGCGTGGT TAGCGACGAG ATCGTGTACC TGACCGCCGA CGAGGAGGAC	360
CGCCACGTGG TGGCACAGGC CAATTCGCCG ATCGATGCGG ACGGTCGCTT CGTCGAGCCG	420
CGCGTGCTGG TCCGCCGCAA GGCGGGCGAG GTGGAGTACG TGCCCTCGTC TGAGGTGGAC	480
TACATGGACG TCTCGCCCCG CCAGATGGTG TCGGTGGCCA CCGCGATGAT TCCCTTCCTG	540
GAGCACGACG ACGCCAACCG TGCCCTCATG GGGGCAAACA TGCAGCGCCA GGCGGTGCCG	600
CTGGTCCGTA GCGAGGCCCC	620

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 620 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

ATCAACATCC	GGCCGGTGGT	CGCCGCGATC	AAGGAGTTCT	TCGGCACCAG	CCAGCTGAGC	60
CAATTCATGG	ACCAGAACAA	CCCCTGTCTG	GGGTTGACCT	ACAAGCGCCG	ACTGTCGGCG	120
CTGGGGCCCCG	GCGGTCTGTC	ACGTGAGCGT	GCCGGGCTGG	AGGTCCGCGA	CGTGCACCCG	180
TCGCACTACG	GCCGGATGTG	CCCCTGCGAA	ACCCCTGAGG	GGCCCAACAT	CGGTCTGATC	240
GGCTCGCTGT	CGGTGTACGC	GCGGGTCAAC	CCGTTCCGGT	TCATCGAAAC	GCCGTACCGC	300
AAGGTGGTCG	ACGGCGTGGT	TAGCGACGAG	ATCGTGTACC	TGACCGCCGA	CGAGGAGGAC	360
CGCCACGTGG	TGGCACAGGC	CAATTCGCCG	ATCGATGCGG	ACGGTCGCTT	CGTCGAGCCG	420
CGCGTGCTGG	TCCGCCGCAA	GGCGGGCGAG	GTGGAGTACG	TGCCCTCGTC	TGAGGTGGAC	480
TACATGGACG	TCTCGCCCCG	CCAGATGGTG	TCGGTGGCCA	CCGCGATGAT	TCCCTTCCTG	540
GAGCACGACG	ACGCCAACCG	TGCCCTCATG	GGGGCAAACA	TGCAGCGCCA	GGCGGTGCCG	600
CTGGTCCGTA	GCGAGGCCCC					620

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 620 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ATCAACATCC	GGCCGGTGGT	CGCCGCGATC	AAGGAGTTCT	TCGGCACCAG	CCAGCTGAGC	60
CAATTCATGG	ACCAGAACAA	CCCCTGTCTG	GGGTTGACCC	ACAAGCGCCG	ACTGTTGGCG	120
CTGGGGCCCCG	GCGGTCTGTC	ACGTGAGCGT	GCCGGGCTGG	AGGTCCGCGA	CGTGCACCCG	180
TCGCACTACG	GCCGGATGTG	CCCCTGCGAA	ACCCCTGAGG	GGCCCAACAT	CGGTCTGATC	240
GGCTCGCTGT	CGGTGTACGC	GCGGGTCAAC	CCGTTCCGGT	TCATCGAAAC	GCCGTACCGC	300
AAGGTGGTCG	ACGGCGTGGT	TAGCGACGAG	ATCGTGTACC	TGACCGCCGA	CGAGGAGGAC	360
CGCCACGTGG	TGGCACAGGC	CAATTCGCCG	ATCGATGCGG	ACGGTCGCTT	CGTCGAGCCG	420
CGCGTGCTGG	TCCGCCGCAA	GGCGGGCGAG	GTGGAGTACG	TGCCCTCGTC	TGAGGTGGAC	480
TACATGGACG	TCTCGCCCCG	CCAGATGGTG	TCGGTGGCCA	CCGCGATGAT	TCCCTTCCTG	540
GAGCACGACG	ACGCCAACCG	TGCCCTCATG	GGGGCAAACA	TGCAGCGCCA	GGCGGTGCCG	600
CTGGTCCGTA	GCGAGGCCCC					620

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GGGGCCTCGC TACGGACCAG CGGCACCGCC TGGCGCTGCA TGTTTGCCCC CATGAGGGCA	60
CGGTTGGCGT CGTCGTGCTC CAGGAAGGGA ATCATCGCGG TGGCCACCGA CACCATCTGG	120
CGGGGCGAGA CGTCCATGTA GTCCACCTCA GACGAGGGCA CGTACTCCAC CTCGCCCCGCC	180
TTGCGGCGGA CCAGCACGCG CGGCTCGACG AAGCGACCGT CCGCATCGAT CGGCGAATTG	240
GCCTGTGCCA CCACGTGGCG GTCCTCCTCG TCGGCGGTCA GGTACACGAT CTCGTCGCTA	300
ACCACGCCGT CGACCACCTT GCGGTACGGC GTTTCGATGA ACCCGAACGG GTTGACCCGC	360
GCGTACACCG ACAGCGAGCC GATCAGACCG ATGTTGGGCC CCTCAGGGGT TTCGATCGGG	420
CACATCCGGC CGTAGTGCGA CGGGTGCACG TCGCGGACCT CCAGCCCGGC ACGCTCACGT	480
GACAGACCGC CGGGCCCCAG CGCCGACAGT CGGCGCTTGT GGGTCAACCC CGACAGCGGG	540
TTGTTCTGGT CCATGAATTG GCTCAGCTGG CTGGTGCCGA AGAACTCCTT GATCGCGGCG	600
ACCACCGGCC GGATGTTGAT	620

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGGGCCTCGC TACGGACCAG CGGCACCGCC TGGCGCTGCA TGTTTGCCCC CATGAGGGCA	60
CGGTTGGCGT CGTCGTGCTC CAGGAAGGGA ATCATCGCGG TGGCCACCGA CACCATCTGG	120
CGGGGCGAGA CGTCCATGTA GTCCACCTCA GACGAGGGCA CGTACTCCAC CTCGCCCCGCC	180
TTGCGGCGGA CCAGCACGCG CGGCTCGACG AAGCGACCGT CCGCATCGAT CGGCGAATTG	240
GCCTGTGCCA CCACGTGGCG GTCCTCCTCG TCGGCGGTCA GGTACACGAT CTCGTCGCTA	300
ACCACGCCGT CGACCACCTT GCGGTACGGC GTTTCGATGA ACCCGAACGG GTTGACCCGC	360
GCGTACACCG ACAGCGAGCC GATCAGACCG ATGTTGGGCC CCTCAGGGGT TTCGATCGGG	420
CACATCCGGC CGTAGTGCGA CGGGTGCACG TCGCGGACCT CCAGCCCGGC ACGCTCACGT	480

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

TTGACCTCCC ACCCGACTTG

20

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA GCGGCATCGA GGTCGTATGG 60
ACGAACACCC CGACGAAATG GGACAACAGT TTCCTCGAGA TCCTGTACGG CTACGAGTGG 120
GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC 180
GGCACCATCC CGGACCCGTT CGGCGGGCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC 240
CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTCGCTGGCT GGAACACCCC 300
GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT 360
CCCGTTGCGA GATACCTTGG GCCGCTGGTC CCCAAGCAGA CCCTGCTGTG GCAGGATCCG 420
GTCCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG 480
ATCCGGGCAT CGGGATTGAC TGTCTCACAG CTAGTTTCGA CCGCATGGGC GGCGGCGTCG 540
TCGTTCCGTG GTAGCGACAA GCGCGGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA 600
CAAGTCGGGT GGGAGGTCAA 620

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA CCGGCATCGA GGTCGTATGG 60
ACGAACACCC CGACGAAATG GGACAACAGT TTCCTCGAGA TCCTGTACGG CTACGAGTGG 120
GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC 180
GGCACCATCC CGGACCCGTT CGGCGGGCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC 240
CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTCGCTGGCT GGAACACCCC 300

GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT	360
CCCGTTGCGA GATACCTTGG GCCGCTGGTC CCCAAGCAGA CCCTGCTGTG GCAGGATCCG	420
GTCCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG	480
ATCCGGGCAT CGGGATTGAC TGTCTCACAG CTAGTTTCGA CCGCATGGGC GGCGGCGTCG	540
TCGTTCCGTG GTAGCGACAA GCGCGGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA	600
CAAGTCGGGT GGGAGGTCAA	620

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA GCGGCATCGA GGTCGTATGG	60
ACGAACACCC CGACGAAATG GGACAACAGT TTCCTCGAGA TCCTGTACGG CTACGAGTGG	120
GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC	180
GGCACCATCC CGGACCCGTT CGGCGGGCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC	240
CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTCGCTGGCT GGAACACCCC	300
GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT	360
CCCGTTGCGA GATACCTTGG GCCGCTGGTC CCCAAGCAGA CCCTGCTGTG GCAGGATCCG	420
GTCCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG	480
ATCCTGGCAT CGGGATTGAC TGTCTCACAG CTAGTTTCGA CCGCATGGGC GGCGGCGTCG	540
TCGTTCCGTG GTAGCGACAA GCGCGGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA	600
CAAGTCGGGT GGGAGGTCAA	620

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA CCGGCATCGA GGTCGTATGG	60
ACGAACACCC CGACGAAATG GGACAACAGT TTCCTCGAGA TCCTGTACGG CTACGAGTGG	120

GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC	180
GGCACCATCC CGGACCCGTT CGGCGGGCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC	240
CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTCGCTGGCT GGAACACCCC	300
GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT	360
CCCGTTGCGA GATACCTTGG GCCGCTGGTC CCCAAGCAGA CCCTGCTGTG GCAGGATCCG	420
GTCCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG	480
ATCCTGGCAT CGGGATTGAC TGTCTCACAG CTAGTTTCGA CCGCATGGGC GCGGCGCTCG	540
TCGTTCCGTG GTAGCGACAA GCGCGGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA	600
CAAGTCGGGT GGGAGGTCAA	620

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCGC	60
TTGTCGCTAC CACGGAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA	120
GTCAATCCCG ATGCCCGGAT CTGGCTCTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG	180
TCGTGGCTGA CCGCAGGGAC CGGATCCTGC CACAGCAGGG TCTGCTTGGG GACCAGCGGC	240
CCAAGGTATC TCGCAACGGG ACCCATGTCT CGGTGGATCA GCTTGTAACA GGCCTTGGCG	300
AACTCGTCGG CCAATTCTC GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC	360
GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCGCCG	420
AACGGGTCCG GGATGGTGCC GGCACCGGCG CCGTCCTTGG CGGTGTATTG CCAAGCGCCA	480
GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC	540
CATTTCGTG GGGTGTTCGT CCATACGACC TCGATGCCGC TGGTGATCGC GTCCTTACCG	600
GTTCCGGTGC CATACGAGCT	620

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCGC	60
TTGTGCGTAC CACGGAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA	120
GTCAATCCCG ATGCCCGGAT CTGGCTCTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG	180
TCGTGGCTGA CCGCAGGGAC CGGATCCTGC CACAGCAGGG TCTGCTTGGG GACCAGCGGC	240
CCAAGGTATC TCGCAACGGG ACCCATGTCT CGGTGGATCA GCTTGTACCA GGCCTTGGCG	300
AACTCGTCGG CCAATTCCTC GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC	360
GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCGCCG	420
AACGGGTCCG GGATGGTGCC GGCACCGGCG CCGTCCTTGG CGGTGTATTG CCAAGCGCCA	480
GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC	540
CATTTGTCG GGGTGTTCGT CCATACGACC TCGATGCCCG TGGTGATCGC GTCCTTACCG	600
GTTCCGGTGC CATACGAGCT	620

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCGC	60
TTGTGCGTAC CACGGAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA	120
GTCAATCCCG ATGCCCGGAT CTGGCTCTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG	180
TCGTGGCTGA CCGCAGGGAC CGGATCCTGC CACAGCAGGG TCTGCTTGGG GACCAGCGGC	240
CCAAGGTATC TCGCAACGGG ACCCATGTCT CGGTGGATCA GCTTGTACCA GGCCTTGGCG	300
AACTCGTCGG CCAATTCCTC GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC	360
GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCGCCG	420
AACGGGTCCG GGATGGTGCC GGCACCGGCG CCGTCCTTGG CGGTGTATTG CCAAGCGCCA	480
GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC	540
CATTTGTCG GGGTGTTCGT CCATACGACC TCGATGCCCG TGGTGATCGC GTCCTTACCG	600
GTTCCGGTGC CATACGAGCT	620

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCGC 60
TTGTCGCTAC CACGGAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA 120
GTCAATCCCG ATGCCAGGAT CTGGCTCTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG 180
TCGTGGCTGA CCGCAGGGAC CGGATCCTGC CACAGCAGGG TCTGCTTGGG GACCAGCGGC 240
CCAAGGTATC TCGCAACGGG ACCCATGTCT CGGTGGATCA GCTTGTACCA GGCCTTGGCG 300
AACTCGTCGG CCAATTCCTC GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC 360
GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCGCCG 420
AACGGGTCCG GGATGGTGCC GGCACCGGCG CCGTCCTTGG CGGTGTATTG CCAAGCGCCA 480
GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC 540
CATTCGTCG GGGTGTTCTG CCATACGACC TCGATGCCGG TGGTGATCGC GTCCTTACCG 600
GTTCCGGTGC CATACGAGCT 620

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

AGAGTTTGAT CCTGGCTCAG 20

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GGCGGACGGG TGAGTAA 17

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

CTGCTGCCTC CCGTAGGAGT

20

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ATGACGTCAA GTCATCATGG CCCTTACGA

29

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GTACAAGGCC CGGGAACGTA TTCACCG

27

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GCAACGAGCG CAACCC

16

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

ATGACGTCAA GTCATCATGG CCCTTA

26

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

AAATTGAAGA GTTTGATCAT GGCTCAGATT GAACGCTGGC GGCAGGCCTA ACACATGCAA	60
GTCGAACGGT AACAGGAAGA AGCTTGCTTC TTTGCTGACG AGTGGCGGAC GGGTGAGTAA	120
TGTCTGGGAA ACTGCCTGAT GGAGGGGGAT AACTACTGGA AACGGTAGCT AATACCGCAT	180
AACGTCGCAA GACCAAAGAG GGGGACCTTC GGGCCTCTTG CCATCGGATG TGCCAGATG	240
GGATTAGCTA GTAGGTGGGG TAACGGCTCA CCTAGGCGAC GATCCCTAGC TGGTCTGAGA	300
GGATGACCAG CCACACTGGA ACTGAGACAC GGTCCAGACT CCTACGGGAG GCAGCAGTGG	360
GGAATATTGC ACAATGGGCG CAAGCCTGAT GCAGCCATGC CGCGTGTATG AAGAAGGCCT	420
TCGGGTTGTA AAGTACTTTC AGCGGGGAGG AAGGGAGTAA AGTTAATACC TTTGCTCATT	480
GACGTTACCC GCAGAAGAAG CACCGGCTAA CTCCGTGCCA GCAGCCGCGG TAATACGGAG	540
GGTGCAAGCG TTAATCGGAA TTACTGGGCG TAAAGCGCAC GCAGGCGGTT TGTTAAGTCA	600
GATGTGAAAT CCCCAGGCTC AACCTGGGAA CTGCATCTGA TACTGGCAAG CTTGAGTCTC	660
GTAGAGGGGG GTAGAATTCC AGGTGTAGCG GTGAAATGCG TAGAGATCTG GAGGAATACC	720
GGTGGCGAAG GCGGCCCCCT GGACGAAGAC TGACGCTCAG GTGCGAAAGC GTGGGGAGCA	780
AACAGGATTA GATACCCTGG TAGTCCACGC CGTAAACGAT GTCGACTTGG AGGTTGTGCC	840
CTTGAGGCGT GGCTTCCGGA GCTAACGCGT TAAGTCGACC GCCTGGGGAG TACGGCCGCA	900
AGGTTAAAAC TCAAATGAAT TGACGGGGGC CCGCACAAGC GGTGGAGCAT GTGGTTTAAT	960
TCGATGCAAC GCGAAGAACC TTACCTGGTC TTGACATCCA CGGAAGTTTT CAGAGATGAG	1020
AATGTGCCTT CGGGAACCGT GAGACAGGTG CTGCATGGCT GTCGTCAGCT CGTGTGTGA	1080
AATGTTGGGT TAAGTCCCGC AACGAGCGCA ACCCTTATCC TTTGTTGCCA GCGGTCCGGC	1140
CGGGAAGTCA AAGGAGACTG CCAGTGATAA ACTGGAGGAA GGTGGGGATG ACGTCAAGTC	1200
ATCATGGCCC TTACGACCAG GGCTACACAC GTGCTACAAT GGCGCATACA AAGAGAAGCG	1260
ACCTCGCGAG AGCAAGCGGA CCTCATAAAG TGCGTCGTAG TCCGGATTGG AGTCTGCAAC	1320
TCGACTCCAT GAAGTCGGAA TCGCTAGTAA TCGTGGATCA GAATGCCACG GTGAATACGT	1380

TCCCGGGCCT TGTACACACC GCCCGTCACA CCATGGGAGT GGGTTGCAAA AGAAGTAGGT	1440
AGCTTAACCT TCGGGAGGGC GCTTACCACT TTGTGATTCA TGACTGGGGT GAAGTCGTAA	1500
CAAGGTAACC GTAGGGGAAC CTGCGGTTGG ATCACCTCCT TA	1542

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

TTTTTATGGA GAGTTTGATC CTGGCTCAGA GTGAACGCTG GCGGCGTGCC TAATACATGC	60
AAGTCGAACG ATGAAGCTTC TAGCTTGCTA GAAGTGGATT AGTGGCGCAC GGGTGAGTAA	120
GGTATAGTTA ATCTGCCCTA CACAAGAGGA CAACAGTTGG AAACGACTGC TAATACTCTA	180
TACTCCTGCT TAACACAAGT TGAGTAGGGA AAGTTTTTCG GTGTAGGATG AGACTATATA	240
GTATCAGCTA GTTGTAAGG TAATGGCTTA CCAAGGCTAT GACGCTTAAC TGGTCTGAGA	300
GGATGATCAG TCACACTGGA ACTGAGACAC GGTCCAGACT CCTACGGGAG GCAGCAGTAG	360
GGAATATTGC GCAATGGGGG AAACCTTGAC GCAGCAACGC CGCGTGAGG ATGACACTTT	420
TCGGAGCGTA AACTCCTTTT CTTAGGGAAG AATTCTGACG GTACCTAAGG AATAAGCACC	480
GGCTAACTCC GTGCCAGCAG CCGCGGTAAT ACGGAGGGTG CAAGCGTTAC TCGGAATCAC	540
TGGGCGTAAA GGGCGCGTAG GCGGATTATC AAGTCTCTTG TGAAATCTAA TGGCTTAACC	600
ATTAAACTGC TTGGGAAACT GATAGTCTAG AGTGAGGGAG AGGCAGATGG AATTGGTGGT	660
GTAGGGGTAA AATCCGTAGA TATACCAAG AATACCCATT GCGAAGGCGA TCTGCTGGAA	720
CTCAACTGAC GCTAAGGCGC GAAAGCGTGG GGAGCAAACA GGATTAGATA CCCTGGTAGT	780
CCACGCCCTA AACGATGTAC ACTAGTTGTT GGGGTGCTAG TCATCTCAGT AATGCAGCTA	840
ACGCATTAAG TGTACCGCCT GGGGAGTACG GTCGCAAGAT TAAACTCAA AGGAATAGAC	900
GGGGACCCGC ACAAGCGGTG GAGCATGTGG TTTAATTCTGA AGATACGCGA AGAACCTTAC	960
CTGGGCTTGA TATCCTAAGA ACCTTTTAGA GATAAGAGGG TGCTAGCTTG CTAGAACTTA	1020
GAGACAGGTG CTGCACGGCT GTCGTCAGCT CGTGTCTGTA GATGTTGGGT TAAGTCCCGC	1080
AACGAGCGCA ACCCAGGTAT TTAGTTGCTA ACGGTTTCGGC CGAGCACTCT AAATAGACTG	1140
CCTTCGTAAG GAGGAGGAAG GTGTGGACGA CGTCAAGTCA TCATGGCCCT TATGCCCAGG	1200
GCGACACACG TGCTACAATG GCATATAGAA TGAGACGCAA TACCGCGAGG TGGAGCAAAT	1260
CTATAAAATA TGTCCCAGTT CGGATTGTTC TCTGCAACTC GAGAGCATGA AGCCGGAATC	1320

GCTAGTAATC GTAGATCAGC CATGCTACGG TGAATACGTT CCCGGGTCTT GTACTCACCG	1380
CCCGTCACAC CATGGGAGTT GATTTCACCTC GAAGCCGGAA TACTAAACTA GTTACCGTCC	1440
ACAGTGGAAT CAGCGACTGG GGTGAAGTCG TAACAAGGTA ACCGTAGGAG AACCTGCGGT	1500
TGGATCACCT CCT	1513

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1555 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

TTTTATGGAG AGTTTGATCC TGGCTCAGGA TGAACGCTGG CGGCGTGCCT AATACATGCA	60
AGTCGAGCGA ACGGACGAGA AGCTTGCTTC TCTGATGTTA GCGGCGGACG GGTGAGTAAC	120
ACGTGGATAA CCTACCTATA AGACTGGGAT AACTTCGGGA AACC GGAGCT AATACCGGAT	180
AATATTTTGA ACCGCATGGT TCAAAAGTGA AAGACGGTCT TGCTGTCACT TATAGATGGA	240
TCCGCGCTGC ATTAGCTAGT TGGTAAGGTA ACGGCTTACC AAGGCAACGA TACGTAGCCG	300
ACCTGAGAGG GTGATCGGCC AACTTGAAC TGAGACACGG TCCAGACTCC TACGGGAGGC	360
AGCAGTAGGG AATCTTCCGC AATGGGCGAA AGCCTGACGG AGCAACGCCG CGTGAGTGAT	420
GAAGGTCTTC GGATCGTAAA ACTCTGTTAT TAGGGAAGAA CATATGTGTA AGTAACTGTG	480
CACATCTTGA CGGTACCTAA TCAGAAAGCC ACGGCTAACT ACGTGCCAGC AGCCGCGGTA	540
ATACGTAGGT GGCAAGCGTT ATCCGGAATT ATTGGGCGTA AAGCGCGCGT AGGCGGTTTT	600
TTAAGTCTGA TGTGAAAGCC CACGGCTCAA CCGTGGAGGG TCATTGGAAA CTGGAAACT	660
TGAGTGCAGA AGAGGAAAGT GGAATTCCAT GTGTAGCGGT GAAATGCGCA GAGATATGGA	720
GGAACACCAG TGGCGAAGGC GACTTTCTGG TCTGTAACTG ACGCTGATGT GCGAAAGCGT	780
GGGGATCAAA CAGGATTAGA TACCCTGGTA GTCCACGCCG TAAACGATGA GTGCTAAGTG	840
TTAGGGGGTT TCCGCCCCCTT AGTGCTGCAG CTAACGCATT AAGCACTCCG CCTGGGGAGT	900
ACGACCGCAA GGTTGAAACT CAAAGGAATT GACGGGGACC CGCACAAGCG GTGGAGCATG	960
TGGTTTAATT CGAAGCAACG CGAAGAACCT TACCAAATCT TGACATCCTT TGACAACTCT	1020
AGAGATAGAG CCTTCCCCCTT CGGGGGACAA AGTGACAGGT GGTGCATGGT TGTCGTCAGC	1080
TCGTGTCGTG AGATGTTGGG TTAAGTCCCG CAACGAGCGC AACCCTTAAG CTTAGTTGCC	1140
ATCATTAAGT TGGGCACTCT AAGTTGACTG CCGGTGACAA ACCGGAGGAA GGTGGGGATG	1200
ACGTCAAATC ATCATGCCCC TTATGATTTG GGCTACACAC GTGCTACAAT GGACAATACA	1260

AAGGGCAGCG	AAACCGCGAG	GTCAAGCAAA	TCCCATAAAG	TTGTTCTCAG	TTCGGATTGT	1320
AGTCTGCAAC	TCGACTACAT	GAAGCTGGAA	TCGCTAGTAA	TCGTAGATCA	GCATGCTACG	1380
GTGAATACGT	TCCCAGGTAT	TGTACACACC	GCCCGTCACA	CCACGAGAGT	TTGTAACACC	1440
CGAAGCCGGT	GGAGTAACCT	TTTAGGAGCT	AGCCGTCGAA	GGTGGGACAA	ATGATTGGGG	1500
TGAAGTCGTA	ACAAGGTAGC	CGTATCGGAA	GGTGCGGCTG	GATCACCTCC	TTTCT	1555

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